

# SEQUENCE LISTING

04/577,304

<110> Ma, Wu-Po  
Lyamichev, Victor I.  
Kaiser, Michael W.  
Lyamicheva, Natalie E.  
Allawi, Hatim T.  
Schaefer, James J.  
Neri, Bruce P.

<120> Improved Enzymes for the Detection of Specific Nucleic Acid Sequences

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<170> PatentIn Ver. 2.0

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ttccccaagg	tgcgggcctg	gattgagaag	accctggagg	agggcaggag	gcgggggtac	2160
gtggagaccc	tcttcggccg	cgggcgctac	gtgcccgacc	tcaacgcccg	ggtgaagagc	2220
gtgcggggagg	cggcggagcg	catggccttc	aacatgcccg	tccagggcac	cgccgccgac	2280

ctcatgaagc tggccatggt gaagctcttc ccccggtnc aggaaatggg ggccaggatg 2340  
ctcctncagg tccacgacga gctggtcttc gagggcccca aagagcgggc ggaggnggtg 2400  
gccgctttgg ccaaggaggt catggagggg gtctatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga tgggggagga ctggctctcc gccaaaggagt ag 2502

<210> 8  
<211> 833  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 8  
Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
1 5 10 15  
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
20 25 30  
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
35 40 45  
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val  
50 55 60  
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala  
65 70 75 80  
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
85 90 95  
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu  
100 105 110  
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys  
115 120 125  
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp  
130 135 140  
Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly  
145 150 155 160  
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
165 170 175  
Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn  
180 185 190  
Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu  
195 200 205  
Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val  
210 215 220  
Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa  
225 230 235 240

Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val  
 245 250 255  
 Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Leu Ala Leu Ala Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa  
 325 330 335  
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu  
 405 410 415  
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg  
 725 730 735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
 770 775 780  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala  
 785 790 795 800  
 Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
 805 810 815  
 Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 820 825 830  
 Xaa

<210> 9  
 <211> 53  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 9  
 uucgcuuucu ucccuuccuu ucucgccacg uucgccggcu uccccguca agc

53

<210> 10  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 10  
acgggggaaag ccggcgaacg tggcgagaaa 30

<210> 11  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 11  
attagaaagg aaggaagaa agcgaa 26

<210> 12  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 12  
acgggggaaag ccggcgaacg tggcgagaaac 30

<210> 13  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 13  
cttgacgggg aaagccggcg aacgtggcgc 30

<210> 14  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 14  
agaaaggaag ggaagaaagc gaa 23

<210> 15

<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 15  
agggagaagg caactggacc gaaggcc

27

<210> 16  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)  
<223> This 5' end has a fluorescein label.

<220>  
<221> misc\_feature  
<222> (35)  
<223> This 3' end is modified with a dideoxynucleotide.

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 16  
ncgaaattaa tacgcttggtg gagaaggagt tcatn

35

<210> 17  
<211> 640  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 17  
gggagcccag cuaugaacuc cuucuccaca agcgccuucg guccaguugc cuucucccug 60  
gggcugcucc ugguguugcc ugcugccuuc ccugccccag uacccccagg agaagauucc 120  
aaagauguag ccgccccaca cagacagcca cucaccucu cagaacgaau ugacaaacaa 180  
auucgguaa uccucgacgg caucucagcc cugagaaagg agacauguaa caagaguaac 240  
augugugaaa gcagcaaaga ggcacuggca gaaaacaacc ugaaccuucc aaagauggcu 300  
gaaaaaagau gaugcuucca aucuggauuc aaugaggaga cuugccuggu gaaaaucauc 360  
acuggucuuu uggaguuga gguauaccua gaguaccucc agaacagauu ugagaguagu 420  
gaggaacaag ccagagcugu ccagaugagu acaaaaagucc ugauccaguu ccugcagaaa 480  
aaggcaaaga aucuagaugc aaauaccacc ccugacccaa ccacaaaugc cagccugcug 540  
acgaagcugc aggcacagaa ccaguggcug caggacauga caacucaucu cauucugcgc 600

agcuuuaagg aguuccugca guccagccug agggcucuuc

640

<210> 18  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 18  
gctatgaact ccttctccac aagcgccttc ggtccagttg ccttctccct ggg 53

<210> 19  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 19  
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
1 5 10 15  
Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu  
20 25 30  
Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp  
35 40 45  
Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met  
50 55 60  
Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser  
65 70 75 80  
Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg  
85 90 95  
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
100 105 110  
Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys  
115 120 125  
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
130 135 140  
Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys  
145 150 155 160  
Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg  
165 170 175  
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
180 185 190  
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
195 200 205



Pro Leu Gly Gln Arg Ile  
210

<210> 20  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 20

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
1 5 10 15  
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
20 25 30  
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
35 40 45  
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
50 55 60  
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
65 70 75 80  
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
85 90 95  
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
100 105 110  
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys  
115 120 125  
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
130 135 140  
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
145 150 155 160  
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
165 170 175  
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
180 185 190  
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
195 200 205  
Pro Leu Gly Gln Arg Ile  
210

<210> 21  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>



acggaacgag cgtctttcat ctgtcaatc

29

<210> 26  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)  
<223> This 5' end is labeled with  
tetrachlororfluorescein.

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 26  
nttttcaact gccgtga

17

<210> 27  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)  
<223> This 5' end is modified with a biotin-streptavitin  
complex.

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 27  
nucacggcag uuggugcgcc ucggaacgag gcgcacg

37

<210> 28  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 28  
tcacggcagt tggcgccct cggaacgagg cgcacg

36

<210> 29  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (30)  
<223> This 3' end is modified with an amine moiety.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 29

cggaggaagc agttggtgcg cctcgttaan

30

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_feature

<222> (1)

<223> This 5' end is labeled with fluorescein.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 30

ntccttctca actgcttcct ccg

23

<210> 31

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_feature

<222> (28)

<223> This 3' end is modified with a biotin moiety.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 31

aacgaggcgc acctcaaadc tccctttn

28

<210> 32

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_feature

<222> (1)

<223> This 5' end is labeled with fluorescein.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 32

nttttcgctg tctcgct

17

<210> 33

<211> 13

<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 33  
acgagcgtct ttg

13

<210> 34  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)  
<223> This 5' end is labeled with fluorescein.

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 34  
nagcgagaca gcgaaagacg ctcgtt

26

<210> 35  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 35  
ucacggcagu uggugcggaa cgcacg

26

<210> 36  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 36  
tcacggcagt tggcgcgaa cgcacg

26

<210> 37  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 37  
cacgaattcg gggatgctgc ccctctttga gcccaa

36

<210> 38  
<211> 34

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 38  
gtgagatcta tcactccttg gcggagagcc agtc 34

<210> 39  
<211> 2502  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 39  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggc caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggcct agggcctttc tggagaggct tgagtttgcc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
gatcttctgg ccctggccgc cgccaggggg ggccgggtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctccgccc gccgacgacc ccattgctcct cgcctacctc 1140  
ctggaccctt ccaacaccac ccccaggggg gtggcccgcc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtgggggagg 1260  
cttgaggggg aggagaggct cctttggcct taccgggagg tggagaggcc cctttccgct 1320

gtcctggccc acatggaggg cacgggggtg cgcctggacg tggcctatct cagggccttg 1380  
 tccctggagg tggccgggga gatcgccgc ctcgaggccg aggtcttcg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tctctttga cgagctaggg 1500  
 cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgaccccttg ccggacctca tccacccag gacgggcccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggacc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 tcccccaagg tgcgggcctg gattgagaag acctggagg agggcaggag gcgggggtac 2160  
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 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccggggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc ccaggttg aggaaatggg ggccaggatg 2340  
 ctcttcagg tccacgacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaggagt ga 2502

<210> 40

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 40

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	

Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		

Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			

Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400



Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750  
Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765  
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780  
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800  
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815  
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu

<210> 41  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 41  
cacgaattcc gaggcgatgc ttccgctc

28

<210> 42  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 42  
tcgacgtcga ctaacccttg gcggaaagcc

30

<210> 43  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 43  
gcatcgcctc ggaattcatg gtc

23

<210> 44  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 44

atagccatgg tggagcggcc gctctcccgg

30

<210> 45

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 45

aagcgtcgac tcaatcctgc ttcgcctcca gcc

33

<210> 46

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 46

aatcgaattc accccacttt ttgacctgga gg

32

<210> 47

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 47

ccgggagagc ggccgctcca c

21

<210> 48

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 48

atggaattca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac 60

ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag 120

ccggtgcaga tggctctacgg cttegcccgg agcctcctca aggccttgaa ggaggacgga 180

caggcgggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag 240

gcctacaagg cgggcccgggc cccacccccg gaggacttcc cccgccagct cgccttggtc 300



tacgtggaga ccctgttcgg caggaggcgc tatgtgcccg acctggcctc cggggtccgc 2220  
 tccgtgcggg aggcggcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgcc 2280  
 gacctgatga agatcgccat ggtcaagctc ttccccaggc taaagcccct gggggcccac 2340  
 ctctctctcc aagtgcacga cgagctggtc ctggagggtgc ccgaggaccg ggccgaggag 2400  
 gccaaagggc tggtaagga ggtcatggag aacgcctacc ccctggacgt gccctcgag 2460  
 gtggagggtg gcgtgggtcg ggactggctg gaggcgaagc aggattga 2508

<210> 49  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 49  
 actggaattc ctgcccctct ttgagcccaa g 31

<210> 50  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 50  
 aacagtcgac ctaggccttg gcggaaagcc 30

<210> 51  
 <211> 2499  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 51  
 atggaattcc tgcccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac 60  
 ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgagg ggagccgggtc 120  
 caggcgggtg acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg 180  
 gtgatcgtgg tgtttgacgc caaggccccc tccttcgcgc accagaccta cgaggcctac 240  
 aaggcggggc gggctccac ccccgaggac tttcccggc agcttgccct tatcaaggag 300  
 atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc 360  
 ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcac cctcaccgcg 420  
 gaccgggacc ttaccagct tctttcgag cgaatctcca tccttcaccc ggagggttac 480

ctgatcacc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac 540  
taccgggcct tggccgggga cccttccgac aacatccccg gcgtgaaggg catcggggag 600  
aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg 660  
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag 720  
ctatccctgg agctatcccc ggtgcacacg gacttgtctc ttcaggtgga cttcgcccgg 780  
cgccgggagc cggaccggga ggggcttaag gcctttttgg agaggctgga gttcggaagc 840  
ctcctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg 900  
cccccgagg gagccttcgt ggggtacgtt ctttcccgc ccgagcccat gtgggcggag 960  
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gccttgccgg ggcttgggga ggtgaggggg cttttggcca aggacctggc ggtgctggcc 1080  
ctgagggaag ggattgccct ggcaccgggc gacgacccca tgctcctcgc ctacctctg 1140  
gatccttcca acaccgcccc cgaaggggta gcccggcgt acggggggga gtggaccgag 1200  
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cctttcaacc tgaactcccc ggaccagctg gaaagggtca tctttgacga gcttgggctt 1500  
cccgccatcg gcaagacgga gaagacgggc aagcgctcca ccagcgccgc cgttttggag 1560  
gccttgccgg aggcctcatcc catcgtggac cgcctccttc agtaccggga gctttccaag 1620  
ctcaaggga cctacatcga tcccttgctt gccctggtcc accccaagac gaaccgcctc 1680  
cacaccggt tcaaccagac ggccaccgcc acggggaggc ttagcagctc ggatcctaata 1740  
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gaggaggggt ggaggctggt ggttttggac tacagccaga ttgagctcag ggtcctggcg 1860  
cacctttccg gggacgagaa cctaaccgg gtcttccagg agggccagga catccacacc 1920  
cagacggcca gctggatgtt cggcgtgccc ccagaggccg tggattccct gatgcgccg 1980  
gcggccaaga ccatcaactt cggcgtcctc tacggcatgt ccgcccaccg gctttcggga 2040  
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gaaaccctct ttggccgccg gcgctacgtg cccgacttgg cttcccgggt gaagagcatc 2220  
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ttgcaggtgc acgacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtcgcc 2400  
caggaggcca agcggaccat ggaggaggtg tggccctga aggtgccctt ggagggtgaa 2460  
gtgggcatcg gggaggactg gctttccgcc aaggcctag 2499

<210> 52  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 52  
cgatctcctc ggccacctcc 20

<210> 53  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 53  
ggcgtgccc tggacgggca 20

<210> 54  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 54  
ccagctcggt gtggacctga 20

<210> 55  
<211> 2505  
<212> DNA  
<213> Thermus aquaticus

<220>  
<221> CDS  
<222> (1)..(2499)

<400> 55  
atg aat tgc ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48  
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag 96  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc 144





ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc	960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc	1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala	
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt	1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	
340 345 350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc	1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu	
355 360 365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc	1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser	
370 375 380	
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg	1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr	
385 390 395 400	
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac	1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn	
405 410 415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg	1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg	
420 425 430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg	1344
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr	
435 440 445	
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg	1392
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val	
450 455 460	
gcc gag gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc	1440
Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly	
465 470 475 480	
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt	1488
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe	
485 490 495	
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag	1536
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys	
500 505 510	
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc	1584
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro	
515 520 525	
atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc	1632
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser	

530	535	540	
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc 1680			
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg			
545 550 555 560			
ctc cac acc cgc ttc aac cag acg gcc acg gcc acg ggc agg cta agt 1728			
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser			
565 570 575			
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg 1776			
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly			
580 585 590			
cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg 1824			
Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val			
595 600 605			
gcc ctg gac tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc 1872			
Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser			
610 615 620			
ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac 1920			
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His			
625 630 635 640			
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac 1968			
Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp			
645 650 655			
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac 2016			
Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr			
660 665 670			
ggc atg tgc gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag 2064			
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu			
675 680 685			
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg 2112			
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val			
690 695 700			
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac 2160			
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr			
705 710 715 720			
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc 2208			
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala			
725 730 735			
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg 2256			
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met			
740 745 750			
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag 2304			
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys			
755 760 765			
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc 2352			
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val			
770 775 780			

cac aac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg 2400  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800

gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg 2448  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815

ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag 2496  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830

gag tgatag 2505  
 Glu

<210> 56  
 <211> 833  
 <212> PRT  
 <213> Thermus aquaticus

<400> 56  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg



Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830

Glu

<210> 57  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 57

caggaggagc tcgttggtgga cctgga

26

<210> 58

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 58

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu

255

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly  
 835

<210> 59

<211> 2511

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 59

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac 60



ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccc acccccgagg acttccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag 360  
gcgacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctctctccg accgcgtcgc cgtcctccac 480  
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
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gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
gacctcgccc aggggcggga gcccgaccg gaggggctta gggccttctt ggagaggctg 840  
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900  
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc 960  
atgtggggcg agcttaaagc cctggccgcc tgcagggacg gccgggtgca ccgggcagca 1020  
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080  
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctcctc 1140  
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gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860  
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920





ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
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 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
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<210> 63  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 63  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
           1                  5                  10                  15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
                   20                  25                  30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
           35                  40                  45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
           50                  55                  60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
           65                  70                  75                  80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
                   85                  90                  95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
           100                  105                  110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
           115                  120                  125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
           130                  135                  140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
           145                  150                  155                  160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
           165                  170                  175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
           180                  185                  190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
           195                  200                  205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 64  
 <211> 2526  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 64

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag 360  
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480  
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag 600  
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttccct ggagaggctg 840  
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900  
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc 960  
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gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctcctc 1140  
gcctacctcc tggaccttc caacaccacc cccgaggggg tggcgcgcg ctacgggggg 1200  
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260  
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caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440  
ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac 1500  
gagcttaggc ttccgcctt ggggaagacg caaaagacag gcaagcgctc caccagcgcc 1560  
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gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccaccgagg 1680  
acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740

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cgcgctctcg cccacctctc cggggacgaa aacctgatca ggggtcttcca ggaggggaag 1920  
gacatccaca ccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc 1980  
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgctc tctacggcat gtccgcccac 2040  
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100  
ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacac caacgcccgg 2220  
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280  
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
gcccgcatgc tcctccaggt ccacaacgag ctctccttgg agggccccca agcgcggggc 2400  
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520  
caccac 2526

<210> 65  
<211> 842  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 65  
Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15  
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30  
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45  
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60  
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80  
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125







Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 66  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 66  
gccgccaggg gcggccgcgt ccaccgggcc 30

<210> 67  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 67  
gcctgcaggg gcggccgcgt gcaccggggc a 31

<210> 68  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 68  
ctcctggacc cttcgaacac cacc 26

<210> 69  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 69  
gtcctggccc atatggaggc cac 23

<210> 70  
<211> 2526  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 70

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccagag acttccccgc gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaaccgcc tcgaggtccc cggctacgag 360  
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctctgtctcg accgcgtcgc cgtcctccac 480  
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600  
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840  
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gccgtcttgg cctcgaggga ggggctagac ctctgtcccc gggacgacct catgctcctc 1140  
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg 1200  
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260  
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gagcttaggc ttccgcctt ggggaagacg caaaagacag gcaagcgctc caccagcgcc 1560  
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gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg 1680  
acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740

tccgacccca acctgcagaa catccccgtc cgcaccccct tgggccagag gatccgccgg 1800  
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860  
cgcgctctcg cccacctctc cggggacgaa aacctgatca ggggtcttcca ggaggggaag 1920  
gacatccaca ccagaccgc aagctggatg ttcggcgtcc ccccgaggc cgtggacccc 1980  
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040  
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100  
ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacac caacgcccgg 2220  
gtgaagagcg tcaggaggc cgcgagcgc atggccttca acatgcccgt ccagggcacc 2280  
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
gcccgcacgc tcctccaggt ccacaacgag ctctcctgg agggccccc agcgcgggcc 2400  
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520  
caccac 2526

<210> 71  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 71  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggctctacg cttcgccaag agcctcctca aggcctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gcccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cccacgcgc gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggc caagggcac 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720

aagctctcct gggacctggc caaggtgcg accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
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gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctccccccc ggcgacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200  
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cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320  
gtcctggccc atatggaggg cacgggggtg cgcttgagcg tggcctatct cagggccttg 1380  
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caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
gtggagaccc tcttcggccg ccgcccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaaggag accaccacca ccaccac 2517

<211> 842  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 72

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75					80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100						105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			





His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly His His His His His His  
 835 840

<210> 73  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 73  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile

60

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 74  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 74  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120  
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cggggcgggg cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840



<220>

<223> Description of Artificial Sequence: Synthetic

<400> 75

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255  
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270  
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285  
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300  
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala



Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800  
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Gly His His His His His His  
 835

<210> 76  
 <211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 76

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240  
 tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300  
 ctcatcaagg agctggtgga cctcctggggg ttaccgccg tgcaggtccc cggctacgag 360  
 gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420





gccgccgacc tcatgaagct ggctatgggtg aagctcttcc ccaggctgga ggaaatgggg 2340  
 gccaggatgc tccttcaggt ccacaacgag ctggctcctcg aggccccaaa agagaggggcy 2400  
 gagggcgtgg cccggctggc caaggaggtc atggagggggg tgtatcccct ggccgtgccc 2460  
 ctggaggtgg aggtggggat aggggaggac tggctctccg ccaaggagca ccaccaccac 2520  
 caccac 2526

<210> 77  
 <211> 842  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 77  
 Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
 1 5 10 15  
 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30  
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45  
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60  
 Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80  
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 85 90 95  
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110  
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125  
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140  
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly  
 355 360 365  
 Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu  
 405 410 415  
 Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp  
 420 425 430  
 Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser  
 450 455 460  
 Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp  
 595 600 605  
 Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg  
 625 630 635 640  
 Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala  
 785 790 795 800  
 Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Glu His His His His His His  
 835 840

<210> 78

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 78

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcbc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200  
gaggacgcgc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320  
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380  
tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500  
cttccgcct tggggaagac gcaaaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560  
gaggccctac gggaggccca cccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620  
aagctcaaga acacctacgt ggacccctc ccaagcctcg tccacccgag gacgggcccgc 1680  
ctccacacc gttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740  
aacctgcaga acatccccgt ccgcaccccc ttgggccaga ggatccgccg ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860

gccacacctt ccggcgacga gaacctgac cggtcttcc aggggggag ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggaccc cctgatgcgc 1980  
 cgggaggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
 caggagctag ccattcccta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaggagc accaccacca ccaccac 2517

<210> 79  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 79  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495





Glu His His His His His  
835

<210> 80  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 80  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtcct tgacgccaaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccttgac cggggacgag tccgacaacc ttcccggggc caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900  
ccccgcgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccagggg gtggcccggc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtggggggagg 1260  
cttgaggggg aggagaggct ctttggctt taccgggagg tggagaggcc ctttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgcttgacg tggcctatct cagggccttg 1380  
tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500

cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
 gaggcctcc gcgaggcca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcgtg 1800  
 gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860  
 gccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac 1920  
 acccagaccg caagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggtctctc 2040  
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100  
 ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160  
 gtggaaaccc tcttcggaag aaggcgctac gtgcccagcc tcaacgcccg ggtgaagagc 2220  
 gtcaggaggc ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcacg 2340  
 ctctccagg tccacaacga gctctcctg gaggccccc aagcgcgggc cgaggaggtg 2400  
 gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460  
 gaggtgggga tgggggagga ctggctttcc gccaaaggct accaccacca ccaccac 2517

<210> 81  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 81  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430

004250"052400

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr	435	440	445
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val	450	455	460
Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly	465	470	475
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe	485	490	495
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys	500	505	510
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro	515	520	525
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser	530	535	540
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg	545	550	555
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser	565	570	575
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly	580	585	590
Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val	595	600	605
Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser	610	615	620
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His	625	630	635
Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp	645	650	655
Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr	660	665	670
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu	675	680	685
Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val	690	695	700
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr	705	710	715
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala	725	730	735
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	740	745	750
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	755	760	765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800  
 Ala Ala Leu Ala Lys Glu Ala Met Gly Lys Ala Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Gly His His His His His His  
 835

<210> 82  
 <211> 2517  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 82  
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cgggccgggc cccacagccg gaggactttc cccggcaact cgccctcatc 300  
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggagggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagagggt tgagtttggc 840  
 agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900  
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
 gcggggctaa aggacctcaa ggaggtccgg ggctcctcgc ccaaggacct cgccgtcttg 1080  
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140

ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200  
gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320  
gtcctggccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380  
tccctggagg tggccgagga gatcgccgcg ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
cttcccgcga tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
gaggccctcc gcgaggccca ccccatcggt gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacgggcccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggcccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct caggggtgctg 1860  
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980  
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaaggag accaccacca ccaccac 2517

<210> 83  
<211> 839  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 83  
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30







Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 84  
 <211> 2517  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 84  
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgcctcatc 300  
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
 ggggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
 agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900  
 cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200  
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtgggggagg 1260  
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320  
 gtcttgccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380  
 tccctggagc ttgcggagga gatccgcgc ctcgaggagg aggtcttccg cttggcgggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500  
 cttcccgcct tggggaagac gcaaaagaca ggcaagcgt ccaccagcgc cgcggtgctg 1560  
 gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620  
 aagctcaaga acacctacgt ggacccccct ccaagcctcg tccaccgag gacgggccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740  
 aacctgcaga acatccccgt ccgcaccccc ttgggcccaga ggatccgcgg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 85  
 <211> 839  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 85

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255  
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270  
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285  
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540  
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His  
 835

<210> 86

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 86

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cgggccgggc cccacgccg gaggacttcc cccggcaact cgccctcatc 300  
 aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
 gggtagctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggagggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
 ccccgccggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200  
 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccg 1320  
 gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380  
 tccctggagc ttgcgaggga gatccgcgc ctcgaggagg aggtcttccg cttggcgggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500  
 cttccgcct tggggaagac gcaaaagaca ggcaagcgt ccaccagcgc cgcggtgctg 1560  
 gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620  
 aagctcaaga acacctacgt ggacccctc ccaagcctcg tccaccgag gacgggccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740  
 aacctgcaga acatccccgt ccgcaccccc ttggggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggag ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
 cggcgggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccc ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280

ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tccacaacga gctggtcctc gagggcccaa aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaggagc accaccacca ccaccac 2517

<210> 87  
<211> 839  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 87  
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540  
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575



Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His  
 835

<210> 88

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 88

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tegtgtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggc cccacgcgc gaggactttc cccggcaact cgcctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcaggg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccgcc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcac 600  
ggggagaaga cggcgaggaa gcttctggag gagggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc cctggagggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg 1020  
gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
gcctcagagg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140  
ctggacctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtgagc 1200  
gaggaggcgg gggagcgggc cgcctttcc gagaggctct tcgccaacct gtgggggagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgt 1320  
gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380  
tccctggagg tggccgagga gatcggccgc ctgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc cggggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
cttcccgcga tcggcaagac ggagaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560  
gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgaccttgg ccggacctca tccacccag gacgggccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgcgg ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920

acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980  
 cgggaggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tccacaacga gctggctctc gagggcccaa aagagagggc ggaggccgtg 2400  
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gcccaaggagc accaccacca ccaccac 2517

<210> 89

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 89

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
						135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145					150				155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	



Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 90  
<211> 2526  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 90  
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaccgccc tcgaggctcc cggtctcgag 360  
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420  
atcctcaccg ccgaccgga cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480  
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600  
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840  
gagttcggca gcctcctcca cgagttcggc ctctggagg ccccgcccc cctggaggag 900  
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccc ccccgagccc 960  
atgtgggcgg agcttaaagc cctggccgcc tgcagggcg gccgcgtgca ccgggcagca 1020  
gacccttg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080  
gccgtcttg cctcgaggga ggggctagac ctctgcccc gggacgaccc catgctcctc 1140  
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg 1200  
gagtggacgg aggacgcgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260  
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgagggt ggaaaagccc 1320  
ctctcccg tctggccca tatggaggcc accggggtac ggcgggacgt ggacctctt 1380  
caggccctt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc 1440  
ttggcgggcc acccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac 1500  
gagcttaggc ttccgcctt ggggaagacg caaaagacag gcaagcgtc caccagcgcc 1560

gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620  
 gagtcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg 1680  
 acgggccgccc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740  
 tccgacccca acctgcagaa catccccgtc cgcacccct tgggccagag gatccgccgg 1800  
 gccttcacg ccgaggaggg gtggctattg gtggccctgg actatagcca gatagagctc 1860  
 aggggtgctgg cccacctctc cggcgacgag aacctgatcc gggctctcca ggaggggagg 1920  
 gacatccaca cggagaccgc cagctggatg ttcggcgctcc cccgggaggc cgtggacccc 1980  
 ctgatgcgcc gggcgcccaa gaccatcaac ttcgggggtcc tctacggcat gtcggccac 2040  
 cgcctctccc aggagctagc catcccttac gaggaggccc aggccttcac tgagcgctac 2100  
 tttcagagct tccccaaagt gcgggcctgg attgagaaga ccctggagga gggcaggagg 2160  
 cgggggtacg tggagaccct cttcgccgc cgcgctacg tgccagacct agaggcccgg 2220  
 gtgaagagcg tgcgggaggc ggccgagcgc atggccttca acatgcccgt ccagggcacc 2280  
 gccgccgacc tcatgaagct ggctatggtg aagctcttcc ccaggctgga ggaaatgggg 2340  
 gccaggatgc tccttcaggt ccacaacgag ctggctctcg agggccaaa agagagggcg 2400  
 gaggccgtgg cccggctggc caaggaggtc atggaggggg tgtatccct ggccgtgccc 2460  
 ctggaggtgg aggtggggat aggggaggac tggctctccg ccaaggagca ccaccaccac 2520  
 caccac 2526

<210> 91

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 91

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65				70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110  
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125  
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140  
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430



Leu 435	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met
Glu 450	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser
Leu 465	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg
Leu 480	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg
Val 495	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys
Thr 510	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu
Ala 525	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys
Leu 540	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg
Thr 555	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly
Arg 570	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr
Pro 585	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp
Leu 600	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala
His 615	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg
Asp 630	Ile	His	Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu
Ala 645	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly
Val 660	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
Pro 675	Tyr	Glu	Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
Pro 690	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg
Arg 705	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
Leu 720	Glu	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
Phe 735	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala

Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala  
785 790 795 800

Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Glu His His His His His His  
835 840

<210> 92  
<211> 2526  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 92  
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag 360  
gcggaacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctctgtctcg accgcgtcgc cgtcctccac 480  
cccaggggccc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600  
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840  
gagttcggca gcctctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900  
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc 960  
atgtgggagg agcttaaagc cctggccgcc tgcaggggag gccgcgtcca ccgggcccc 1020  
gagccttata aagccctcag ggacctgaag gaggcgaggg ggcttctcgc caaagacctg 1080  
agcgttctgg ccctgaggga aggccttggc ctcccgcccc gcgacgacct catgctcctc 1140

gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcccggcg ctacggcggg 1200  
gagtggacgg aggaggcggg ggagcgggcc gccctttccg agaggctctt cgccaacctg 1260  
tgggggaggg ttgaggggga ggagaggctc ctttggtttt accgggaggt ggagaggccc 1320  
ctttccgctg tcctggccca tatggaggcc acgggggtgc gcctggacgt ggcctatctc 1380  
agggccttgt ccctggaggt ggccgaggag atcgcccgcc tcgaggccga ggtcttccgc 1440  
ctggccggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt cctctttgac 1500  
gagctagggc ttcccgccat cggcaagacg gagaagaccg gcaagcgctc caccagcgcc 1560  
gccgtcctgg agggcctccg cgaggccccc cccatcgtag agaagatcct gcagtaccgg 1620  
gagctcacca agctgaagag cacctacatt gacccttgc cggacctcat ccaccccagg 1680  
acgggcccgc tccacaccg cttcaaccag acggccacgg ccacgggcag gctaagtagc 1740  
tccgatccca acctccagaa catccccgtc cgcacccgc ttgggcagag gatccgcccg 1800  
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860  
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctcttcca ggaggggaag 1920  
gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgaggc cgtggacccc 1980  
ctgatgcgcc gggcgccaa gacgggtgaac ttcggcgctc tctacggcat gtccgcccac 2040  
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100  
ttccaaagct tccccagggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacac caacgcccgg 2220  
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccg ccagggcacc 2280  
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
gcccgcacgc tcctccaggt ccacaacgag ctctccttgg agggccccc agcgcgggcc 2400  
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520  
caccac 2526

<210> 93  
<211> 842  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 93  
Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15  
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu

00577204-05240

20					25					30					
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65					70					75				80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
	145					150					155				160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
	225					230					235				240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro
	305					310					315				320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val
				325					330					335	
His	Arg	Ala	Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala
			340					345					350		



Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly His His His His His His  
 835 840

<210> 94  
 <211> 2499  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 94  
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60  
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggccctacggg 240  
 ggggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
 aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc 420  
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcac 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660

aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga gggccccctgg 900  
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
 gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgccacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcgccgg gctacggggg ggagtggacg 1200  
 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccg 1320  
 gtccctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380  
 tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500  
 cttccgcct tggggaagac gcaaaagaca ggcaagcgt ccaccagcgc cgcggtgctg 1560  
 gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620  
 aagctcaaga acacctacgt ggacccccct ccaagcctcg tccaccgag gacgggccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740  
 aacctgcaga acatccccgt ccgcaccccc ttgggcccaga ggatccgccg ggccttcgtg 1800  
 gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860  
 gcccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac 1920  
 acccagaccg caagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040  
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100  
 ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160  
 gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc 2220  
 gtcaggaggg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcatg 2340  
 ctctccagg tccacgacga gctcctcctg gaggcccccc aagcgcgggc cgaggaggtg 2400  
 gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460  
 gaggtgggga tgggggagga ctggccttcc gccaaagggt 2499

<210> 95  
 <211> 833  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 95

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
	225				230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			



Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
290						295					300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
				325					330					335	
Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu
			340					345					350		
Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu
		355					360					365			
Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
	370					375					380				
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr
385					390					395					400
Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn
				405					410					415	
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His
			420					425					430		
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr
		435					440					445			
Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Leu
	450					455					460				
Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly
465					470					475					480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
			485					490						495	
Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys	Thr	Gly	Lys
			500					505					510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro
		515				520						525			
Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn
	530					535					540				
Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg
545					550					555					560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser
				565				570						575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly
			580					585					590		
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val
		595					600					605			
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser
	610					615					620				

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800  
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830

Gly

<210> 96  
 <211> 2499  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 96  
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60  
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120  
 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cggggccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300



gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgccccgagg cggccgagcg catggccttc aacatgcccc tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
 ctcccttcagg tccacgacga gctggctctc gaggcccca aagagagggc ggaggccgtg 2400  
 gccccgctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggag 2499

<210> 97  
 <211> 833  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 97  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg



Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	625	630	635	640
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	705	710	715	720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	725	730	735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	740	745	750	
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	755	760	765	
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	770	775	780	
His	Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	785	790	795	800
Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	805	810	815	
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	820	825	830	

Glu

<210> 98  
 <211> 2499  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 98

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960  
gatctttctg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccattgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccaggggg gtggcccggc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtgggggagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgcttgagc tggcctatct cagggccttg 1380  
tccctggagg tggccgagga gatcggccgc ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
cttcccgcga tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgaccttgg ccggacctca tccaccccag gacgggccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740

aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcgtg 1800  
 gccgagggcg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860  
 gcccacctct ccggggacga aaacctgata agggctcttc aggaggggaa ggacatccac 1920  
 acccagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040  
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100  
 ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160  
 gtggaaaccc tcttcggaag aaggcgctac gtgcccagacc tcaacgcccg ggtgaagagc 2220  
 gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcagc 2340  
 ctctccagg tccacgacga gctcctctg gagggccccc aagcggggc cgaggaggtg 2400  
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460  
 gaggtgggga tgggggagga ctggctttcc gccaaagggt 2499

<210> 99  
 <211> 833  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 99  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140



Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
		180						185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265						270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
			325						330					335	
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu
			340					345					350		
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu
		355					360					365			
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
	370					375					380				
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr
385					390					395					400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn
			405					410						415	
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg
			420					425					430		
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr
		435					440					445			
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
	450					455					460				
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly
465					470					475					480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800  
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
 805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Gly

<210> 100  
<211> 2499  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 100  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120  
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgcctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggc caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggcctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccttttcc gagaggctct tcgccaacct gcttaagagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgcttgagc tggcctatct cagggccttg 1380





Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu

<210> 102

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 102

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caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc ctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900  
ccccgcgcgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020





Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350





aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatacctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcg accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcccgcc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccctttcc gagaggctcc atcggaacct gtgggggagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320  
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380  
tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500  
cttcccgcct tggggaagac gcaaaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560  
gaggccctac gggaggccca ccccatcgct gagaagatcc tccagcaccg ggagctcacc 1620  
aagctcaaga acacctacgt ggacccctc ccaagcctcg tccaccgag gacgggccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740  
aacctgcaga acatccccgt ccgcaccccc ttggggcaga ggatccgccg ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160

gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccc tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggtctg aggaaatggg ggccaggatg 2340  
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 106  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 106  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
     1                    5                    10                    15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
           20                    25                    30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
           35                    40                    45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
       50                    55                    60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
       65                    70                    75                    80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
           85                    90                    95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
           100                    105                    110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
       115                    120                    125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
       130                    135                    140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
       145                    150                    155                    160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
           165                    170                    175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
           180                    185                    190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
       195                    200                    205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg

210	215	220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235 240		
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 255		
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 260 265 270		
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu 275 280 285		
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu 290 295 300		
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala 305 310 315 320		
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala 325 330 335		
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu 340 345 350		
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu 355 360 365		
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser 370 375 380		
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr 385 390 395 400		
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu His Arg Asn 405 410 415		
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg 420 425 430		
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr 435 440 445		
Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu 450 455 460		
Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly 465 470 475 480		
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 495		
Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys 500 505 510		
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 525		
Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn 530 535 540		

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 107

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 107

ctttccgaga ggctccatcg gaacctgtgg gggagg

36

<210> 108

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 108

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag cgggggggag 120  
cgggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcgggtga tcgtgggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
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cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccggcc ggcgacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccagggg gtggcccgcc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
cttgaggggg aggagaggct ctttggctt taccgggagg tggagaggcc ctttccgct 1320  
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380



tccctggagc ttgcgaggga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaagggt tgctctttga cgagcttagg 1500  
 cttcccgct tggggaagac gcaaaagaca ggcaagcgt ccaccagcgc cgcggtgctg 1560  
 gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620  
 aagctcaaga acacctacgt ggacccccctc ccaagcctcg tccacccgag gacggggcgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740  
 aacctgcaga acatccccgt ccgcaccccc ttggggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggacc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagacc ttttcggccg ccgcgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgcgcggac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaggagc accaccacca ccaccac 2517

<210> 109

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 109

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80





Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 110  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 110  
ctcttcgccca acctgcttaa gaggcttgag ggggag 36

<210> 111  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 111  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggc cccacgccg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccgcc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660





Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540  
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 113

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 113

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27

<210> 114

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic



**Abstract** The purpose of this study was to determine the effect of a 12-week training program on the physical fitness of 10-year-old children. The study was conducted in a primary school in Ankara, Turkey. The children were divided into two groups: a control group and an experimental group. The experimental group participated in a 12-week training program that included aerobic, strength, and flexibility exercises. Physical fitness was measured using a series of tests, including a 1000m run, a 15m shuttle run, a 1min sit-up test, a 1min plank test, and a 1min side plank test. The results showed that the experimental group had significantly higher scores than the control group in all tests. The 12-week training program had a positive effect on the physical fitness of 10-year-old children.



gccacacctt cggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
 cggcgggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040  
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 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
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<210> 115  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 115  
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 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495

Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	
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Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	
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Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	
	530					535					540					
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	
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Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565					570					575		
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	
			580					585					590			
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	
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Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	
	610					615					620					
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	
625				630						635					640	
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	
				645					650					655		
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	
			660					665					670			
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	
		675					680					685				
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	
	690					695					700					
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	
705					710					715					720	
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	
				725					730					735		
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	
			740					745					750			
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	
		755					760					765				
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	
	770					775					780					
His	Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	
785					790					795					800	
Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	
				805					810					815		
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	
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Glu His His His His His His  
835

<210> 116  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 116  
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<210> 117  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

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ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtcct tgacgccaaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccggggc ccccaacgccg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggc caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgctacatc 1140



Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
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 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
           50                          55                  60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
   65                          70                  75                  80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
                   85                  90                  95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
                   100                  105                  110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
           115                  120                  125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
   130                  135                  140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
  145                  150                  155                  160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
                   165                  170                  175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
           180                  185                  190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
           195                  200                  205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
   210                  215                  220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
  225                  230                  235                  240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
           245                  250                  255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
           260                  265                  270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
   275                  280                  285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
  290                  295                  300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
  305                  310                  315                  320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
           325                  330                  335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
           340                  345                  350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
           355                  360                  365

Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	
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Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
385					390					395					400	
Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn	
				405					410					415		
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His	
			420					425					430			
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
		435					440					445				
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	
450						455					460					
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	
465					470					475					480	
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
			485						490					495		
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	
			500					505						510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	
		515					520					525				
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	
530						535					540					
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	
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Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565				570						575		
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	
			580					585					590			
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	
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Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	
		610				615					620					
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	
625					630					635					640	
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	
				645					650					655		
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	
			660					665					670			
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	
		675					680					685				
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	
		690				695					700					



Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 119

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 119

gtggcctatc tccaggcctt gtcctg

27

<210> 120

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 120

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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240

gggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420



1. *How long have you been with the company?*  
 2. *What is your current role?*  
 3. *What are your responsibilities in this role?*  
 4. *How do you see your career growing here?*  
 5. *What are your strengths and weaknesses?*  
 6. *What motivates you to work hard?*  
 7. *How do you handle stress and pressure?*  
 8. *What are your future goals?*  
 9. *Do you have any questions for me?*  
 10. *Thank you for your time.*

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<220>
<223> Description of Artificial Sequence: Synthetic
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253

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
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 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 122

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 122

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<210> 123  
 <211> 2517  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

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 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
 aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
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 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccttgagggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
 ccccgccggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960  
 gatcttcttg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
 gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200  
 gaggacgcgc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320  
 gtctggcccc atatggagge cacgggggtg cgcttgagc tggcctatct cagggccttg 1380  
 tccttgagg tggccgagga gatccgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
 cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560

0047304 052400

gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga taggggagga ctggctctcc gcccaaggagc accaccacca ccaccac 2517

<210> 124  
<211> 839  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 124  
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445







agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
 gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200  
 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320  
 gtccctggccc atatggaggc cacgggggtg cgccctggacg tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgccgc ctcgaggagg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
 cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
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 aagctgaaga gcacctacat tgacccttg ccggacctca tccaccag gacgggccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gccgggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggag accaccacca ccaccac 2517

<210> 127  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 127

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255  
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270  
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285  
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300  
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

00430 402450

305	310	315	320
Asp Leu Leu Ala	Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala		
	325	330	335
Ala Asp Pro Leu	Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu		
	340	345	350
Leu Ala Lys Asp	Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu		
	355	360	365
Val Pro Gly Asp	Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser		
	370	375	380
Asn Thr Thr Pro	Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr		
	385	390	400
Glu Asp Ala Ala	His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn		
	405	410	415
Leu Leu Lys Arg	Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His		
	420	425	430
Glu Val Glu Lys	Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr		
	435	440	445
Gly Val Arg Leu	Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val		
	450	455	460
Ala Glu Glu Ile	Ala Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly		
	465	470	475
His Pro Phe Asn	Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe		
	485	490	495
Asp Glu Leu Gly	Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys		
	500	505	510
Arg Ser Thr Ser	Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro		
	515	520	525
Ile Val Glu Lys	Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser		
	530	535	540
Thr Tyr Ile Asp	Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg		
	545	550	555
Leu His Thr Arg	Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser		
	565	570	575
Ser Ser Asp Pro	Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly		
	580	585	590
Gln Arg Ile Arg	Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val		
	595	600	605
Ala Leu Asp Tyr	Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser		
	610	615	620
Gly Asp Glu Asn	Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His		
	625	630	635
			640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
                     645                    650                    655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
                     660                    665                    670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
                     675                    680                    685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
                     690                    695                    700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
                     705                    710                    715                    720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
                     725                    730                    735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
                     740                    745                    750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
                     755                    760                    765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
                     770                    775                    780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
                     785                    790                    795                    800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
                     805                    810                    815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
                     820                    825                    830  
 Glu His His His His His His  
                     835

<210> 128

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 128

gccccgctcg aggaggaggt cttccgc

27

<210> 129

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 129

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60



acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggaccc cctgatgcgc 1980  
 cgggcgccca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040  
 caggagctag ccattccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgcccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tccacaacga gctggctctc gagggcccaa aagagagggc ggaggccgtg 2400  
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 130

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 130

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	



Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510



<210> 131  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 131  
tttgacgagc taaggcttcc cgccatc

27

<210> 132  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 132  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc ctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caagggtgcg accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900  
ccccgcgcg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
gcctcgaggg aggggctaga cctcgtgcc ggggacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccagggg gtggcgcggc gctacggggg ggagtggacg 1200



Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 134  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 134  
atcgccaaga cgcaaaagac cggcaag

27

<210> 135  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 135  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccacccccgag 480

gggtagctca tcaccccgcc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcmc accgacctgc ccttgagggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagagggt tgagtttggc 840  
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 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
 gcggggctaa aggacctcaa ggaggtccgg ggccctctcg ccaaggacct cgccgtcttg 1080  
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgccacctc 1140  
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 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcmc 1260  
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccg 1320  
 gtcctggccc atatggaggc cacgggggtg cgccctggac tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
 cttcccgcca tcggcaagac ggagaagacc ggcaagcgtc ccaccagcmc cgccgtcctg 1560  
 gaggcctcc gcgaggccca ccccatcgtg gagaagatcc tgcagcaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgacccttg ccggacctca tccaccag gacgggcmc 1680  
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 aacctcaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
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 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggag ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggacc cctgatcmc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 tccccaaagg tgcgggctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagacc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagc catggccttc aacatgccc tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340



ctccttcagg tccacaacga gctggtcctc gagggcccaa aagagagggc ggaggccgtg 2400  
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 136  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 136  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu

255

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His  
 835

<210> 137

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 137

aagatcctgc agcaccggga gctcacc

27

<210> 138  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 138  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200  
gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320  
gtcctggccc atatggagge cacgggggtg cgcctggacg tggcctatct cagggccttg 1380  
tccctggagg tggccgagga gatcgccgcg ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560

gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga acacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
gtggagaccc tcttcggccg ccgcgcctac gtgccagacc tagaggcccg ggtgaagagc 2220  
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgcgcgcgac 2280  
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tccacaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
gccccgctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga taggggagga ctggctctcc gcccaaggagc accaccacca ccaccac 2517

<210> 139

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 139

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5				10						15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
		50				55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
		65			70				75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		



0043889"49644"66440

Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	450	455	460	
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	530	535	540	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	625	630	635	640
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	705	710	715	720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	725	730	735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	740	745	750	
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	755	760	765	
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	770	775	780	

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His  
835

<210> 140

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 140

accaagctga agaacaccta cattgac

27

<210> 141

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 141

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cggggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840



agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
 cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
 gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200  
 gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccg 1320  
 gtccctggccc atatggaggc cacgggggtg cgccctggacg tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgcccgc ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
 cttcccgcga tcggcaagac ggagaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560  
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacgt ggacccttg ccggacctca tccaccag gacgggccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcggcca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgccccgagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tccacaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gccgggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggag accaccacca ccaccac 2517

<210> 142  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 142

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255  
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270  
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285  
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300  
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala



Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His  
 835

<210> 143

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 143

aagagcacct acgtggaccc cttgccg

27

<210> 144

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 144

atgaattcgg ggatgctgcc cctctttgag cccaagggcc ggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcttacggg 240  
 gggtagaagg cgggccgggg ccccacgccg gaggactttc cccggcaact cgccctcatc 300  
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
 gggtagctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg 1020  
 gcgggggctaa aggacctcaa ggaggctcgg ggcctcctcg ccaaggacct cgccgtcttg 1080  
 gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200  
 gaggacgccg ccacccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
 ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccg 1320  
 gtctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
 cttcccgcca tcggcaagac ggagaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560  
 gaggccctcc gcgaggcca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgacccttg ccgagcctcg tccacccag gacgggccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctcaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggag ggacatccac 1920

acggagaccg ccagctggat gttcggcgtc ccccgaggagg cagtggaccc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
 ctctttcagg tccacaacga gctggctctc gaggcccca aagagagggc ggaggccgtg 2400  
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 145

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 145

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
						135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	



Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835



<210> 146  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 146  
attgaccctt tgccgagcct cgtccacccc aggacgggc

39

<210> 147  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 147  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
gggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caagggtgcg accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
ccccgcgcgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccatgctcct cgctacctc 1140  
ctggaccctt cgaacaccac ccccaggggg gtggcccgcc gctacggcgg ggagtggacg 1200

gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380  
tccctggagg tggccgagga gatcgcccg ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
cttcccgcga tcggcaagac gcaaaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggacc cctgatgcgc 1980  
cgggcgccca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
gtggagacc tcttcggccg ccgcgctac gtgccagacc tagaggccc ggtgaagagc 2220  
gtgcgggagg cggccgagcg catggccttc aacatgccc tccagggcac cgccgccgac 2280  
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tcacaaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 148

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 148

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5				10						15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20					25						30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
	35					40						45			

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	385	390	395	400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	405	410	415	
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	420	425	430	
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	435	440	445	
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	450	455	460	
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Gln	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	530	535	540	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	625	630	635	640
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	705	710	715	720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 149

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 149

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120

ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240

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gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420

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<210> 150  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 150

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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255  
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270  
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285  
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300  
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

305		310		315		320
Asp Leu Leu Ala	Leu Ala Ala Ala Arg	Gly Gly Arg Val His Arg Ala				
	325		330		335	
Pro Glu Pro Tyr	Lys Ala Leu Arg Asp	Leu Lys Glu Ala Arg Gly Leu				
	340		345		350	
Leu Ala Lys Asp	Leu Ser Val Leu Ala Leu Arg	Glu Gly Leu Gly Leu				
	355		360		365	
Pro Pro Gly Asp	Asp Pro Met Leu Leu Ala Tyr	Leu Leu Asp Pro Ser				
	370		375		380	
Asn Thr Thr Pro	Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr					
	385		390		395	400
Glu Glu Ala Gly	Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn					
	405		410		415	
Leu Leu Gly Arg	Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg					
	420		425		430	
Glu Val Glu Arg	Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr					
	435		440		445	
Gly Val Arg Leu	Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val					
	450		455		460	
Ala Glu Glu Ile	Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly					
	465		470		475	480
His Pro Phe Asn	Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe					
	485		490		495	
Asp Glu Leu Gly	Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys					
	500		505		510	
Arg Ser Thr Ser	Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro					
	515		520		525	
Ile Val Glu Lys	Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser					
	530		535		540	
Thr Tyr Ile Asp	Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg					
	545		550		555	560
Leu His Thr Arg	Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser					
	565		570		575	
Ser Ser Asp Pro	Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly					
	580		585		590	
Gln Arg Ile Arg	Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val					
	595		600		605	
Ala Leu Asp Tyr	Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser					
	610		615		620	
Gly Asp Glu Asn	Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His					
	625		630		635	640







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<210> 153

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 153

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
405 410 415

Leu Trp Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys  
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His  
 835

1. The first part of the report, "Introduction", discusses the importance of the study and the objectives of the research. It also mentions the scope of the study and the limitations.

2. The second part, "Literature Review", provides a comprehensive overview of the existing research on the topic. It identifies the gaps in the current knowledge and highlights the contributions of the study.

3. The third part, "Methodology", describes the research design, data collection methods, and the statistical analysis used in the study. It also includes a discussion on the reliability and validity of the data.

4. The fourth part, "Results", presents the findings of the study. It includes a detailed analysis of the data and a comparison with the existing literature.

5. The fifth part, "Conclusion", summarizes the main findings of the study and discusses the implications for future research. It also provides recommendations for practice.

6. The final part, "References", lists the sources used in the study. It includes a mix of primary and secondary sources, as well as books, journal articles, and online resources.

<400> 154  
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<210> 155
<211> 835
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 155  
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1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu  
20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe  
35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu  
100 105 110

Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys  
115 120 125

Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg  
130 135 140

Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp  
145 150 155 160

Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro  
165 170 175

Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp  
180 185 190

Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu  
195 200 205

Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg

004230 402200

210	215	220
Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp 225 230 235 240		
Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu 245 250 255		
Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly 260 265 270		
Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu 275 280 285		
Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro 290 295 300		
Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro 305 310 315 320		
Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Glu Gly Arg Val 325 330 335		
His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala 340 345 350		
Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly 355 360 365		
Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu 370 375 380		
Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly 385 390 395 400		
Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu 405 410 415		
Phe Gln Asn Leu Phe Pro Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr 420 425 430		
Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala 435 440 445		
Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu 450 455 460		
Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala 465 470 475 480		
Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu 485 490 495		
Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Glu Lys Thr Gly 500 505 510		
Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His 515 520 525		
Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys 530 535 540		

Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly  
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
580 585 590

Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu  
595 600 605

Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
610 615 620

Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile  
625 630 635 640

His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val  
645 650 655

Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr  
675 680 685

Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
690 695 700

Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly  
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala  
725 730 735

Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val  
755 760 765

Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln  
770 775 780

Val His Asp Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu  
785 790 795 800

Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp  
805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala  
820 825 830

Lys Gln Asp  
835

<210> 156

<211> 2526

<212> DNA

<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence: Synthetic

<400> 156

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 ctgatgcgcc gggcgccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040  
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 ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacac caacgcccgg 2220  
 gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280  
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
 gcccgcatgc tcttcaggt ccacaacgag ctctcctggt agggccccca agcgcggggc 2400  
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520  
 caccac 2526

<210> 157

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 157

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65				70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85					90						95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100					105						110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140  
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys  
500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
625 630 635 640

Asp Ile Ala Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 158

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 158

gcttgcggtc tgggtggcga tgccttccc etc

33

<210> 159

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 159

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaaccgcc tcgagggtccc cggctacgag 360  
gcgagcgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctctgtctcg accgcgtcgc cgtcctccac 480  
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag 600  
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcc cctggagggtg 840  
gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgccc cctggaggag 900  
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc 960



<400> 160

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15  
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30  
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45  
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60  
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80  
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125  
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240  
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255  
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
260 265 270  
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
275 280 285  
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val

004360 404 004400

325										330					335				
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val				
			340					345					350						
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly				
		355					360					365							
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu				
	370					375					380								
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly				
	385				390					395					400				
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu				
				405					410					415					
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp				
			420					425					430						
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met				
		435					440					445							
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser				
		450				455					460								
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg				
	465				470						475				480				
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg				
				485				490						495					
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys				
			500					505					510						
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu				
		515					520					525							
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys				
	530					535					540								
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg				
	545				550						555				560				
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly				
				565					570					575					
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr				
			580					585					590						
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp				
		595					600					605							
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala				
		610				615					620								
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys				
	625				630						635				640				
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu				
				645					650					655					



Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Ala Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 161  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 161  
catgttgaag gccatggcct ccgcggcctc cct

33

<210> 162  
<211> 2526  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 162  
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240  
 tacgaggcct acaaggcggg gagggccccc acccccagg acttcccccg gcagctcgcc 300  
 ctcatcaagg agctggtgga cctcctggggg tttacccgcc tcgagggtccc cggctacgag 360  
 gcggaacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtgcgc 420  
 atcctcaccg ccgaccgca cctctaccaa ctctgtctccg accgcgtcgc cgtcctccac 480  
 cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
 cagtgggtgg acttccgcgc cctcgtggggg gacccctccg acaacctccc cgggggtcaag 600  
 ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
 ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
 gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
 gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840  
 gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgccc cctggaggag 900  
 gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctcccg ccccgagccc 960  
 atgtggggcg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca 1020  
 gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080  
 gccgtcttgg cctcgaggga ggggctagac ctctgtcccg gggacgacc catgctcctc 1140  
 gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgcg ctacgggggg 1200  
 gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260  
 cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320  
 ctctcccggg tcttgccca tatggaggcc accggggtac ggcgggacgt ggcctacctt 1380  
 caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440  
 ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac 1500  
 gagcttaggc ttccgcctt ggggaagacg caaaagacag gcaagcgctc caccagcgcc 1560  
 gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620  
 gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccaccgagg 1680  
 acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740  
 tccgaccca acctgcagaa catccccgtc cgcacccctc tgggccagag gatccgccgg 1800  
 gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860  
 cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920  
 gacatccaca ccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980

ctgatgcgcc gggcgcccaa gacggtgaac ttcggcgctcc tctacggcat gtccgcccac 2040  
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100  
 ttccaaagct tcccgaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgcact caacgcccgg 2220  
 gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280  
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
 gcccgcacgc tcctccaggt cgccaacgag ctctccttgg agggccccca agcgcgggcc 2400  
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520  
 caccac 2526

<210> 163

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 163

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65				70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100						105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
	145				150					155				160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly His His His His His His  
 835 840

<210> 164  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 164  
caggaggagc tcgttggcga cctggaggag

30

<210> 165  
<211> 2526  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 165  
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaccgccg tcgaggtccc cggctacgag 360  
gcggaacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420  
atcctcaccg ccgaccgca cctctacca ctctctccg accgcgtcgc cgtcctccac 480  
cccagggggc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600  
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
gacctcgccc aggggcgggg gcccgaccgg gaggggctta gggccttcct ggagaggctg 840  
gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgcccc cctggaggag 900  
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960  
atgtgggagg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca 1020  
gacccttgga cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080  
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctcctc 1140  
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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65				70					75					80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro
305					310					315					320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val
				325					330					335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val
			340					345					350		
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly
		355					360					365			



Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 167  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 167  
ggagcgcttg cctgtcttct tcgtcttctt caaggcgga ggcct 45

<210> 168  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 168  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120  
ccggtgcagg cggcttacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cccacgccc gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccacccccgag 480  
 ggggtacctca tcacccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttccccgggt caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgctc accgacctgc ccctggaggt ggacttcgcc 780  
 aaaaggcggg agccccgacc ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
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 cccccgccgg aaggggcctt cgtgggcctt gtgctttccc gcaaggagcc catgtgggcc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
 aaagccctca gggacctgaa ggaggcgagg gggccttctc ccaaagacct gagcgttctg 1080  
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140  
 ctggaccctt cgaacaccac ccccagggg gtggcccgcc gctacggcgg ggagtggacg 1200  
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
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 gtcttgccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
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 cttcccgcca tcggcaagac gcaaaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
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 gccacctct ccggcgacga gaacctgac cggtcttcc aggaggggcg ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggacct cctgatgcgc 1980  
 cgggcgggca agaccatcaa cttcggggtc ctctacggca tgtcggecca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagacct tcttcggccg ccgccgtac gtgccagacc tagaggcccc ggtgaagagc 2220  
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ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tcgccaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 169  
<211> 839  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 169  
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 170

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 170

gaggaccagc tcgttggcga cctgaaggag cat

33

<210> 171  
 <211> 2517  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 171

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ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240
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aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc tcccgggggt caagggcatc 600
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aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggagggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
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gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260
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tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500
cttcccgcca tcggcaagac gcaaaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560

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gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgaccccttg ccggacctca tccacccag gacgggccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggcg ggacatcgcc 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
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ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
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gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
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gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 172

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 172

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85						90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105						110	







Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 173  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 173  
gaggggaggggg acatcgccac ggagaccgcc agc 33

<210> 174  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 174  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggg cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600  
gggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc cctggagggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggcctt agggcctttc tggagaggct tgagtttggc 840

agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
ccccgcgagg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
gatcttcttg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgagg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380  
tccctggagg tggccgagga gatcgcccgc ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
cttcccgcca tcggcaagac gcaaaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacgggcccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt cgccaccccg cttgggcaga ggatccgccc ggccttcatc 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
gtggagacc tcttcggccg ccgcccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400  
gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaggagc accaccacca ccaccac 2517

<210> 175  
<211> 839  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 175

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255  
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270  
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285  
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300  
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

305		310		315		320
Asp Leu Leu Ala	Leu Ala Ala Ala Arg	Gly Gly Arg Val His Arg Ala				
	325		330		335	
Pro Glu Pro Tyr	Lys Ala Leu Arg Asp	Leu Lys Glu Ala Arg Gly Leu				
	340		345		350	
Leu Ala Lys Asp	Leu Ser Val Leu Ala Leu Arg	Glu Gly Leu Gly Leu				
	355		360		365	
Pro Pro Gly Asp	Asp Pro Met Leu Leu Ala Tyr	Leu Leu Asp Pro Ser				
	370		375		380	
Asn Thr Thr Pro	Glu Gly Val Ala Arg Arg	Tyr Gly Gly Glu Trp Thr				
	385		390		395	
Glu Glu Ala Gly	Glu Arg Ala Ala Leu Ser	Glu Arg Leu Phe Ala Asn				
	405		410		415	
Leu Leu Lys Arg	Leu Glu Gly Glu Glu Arg	Leu Leu Trp Leu Tyr Arg				
	420		425		430	
Glu Val Glu Arg	Pro Leu Ser Ala Val Leu Ala His	Met Glu Ala Thr				
	435		440		445	
Gly Val Arg Leu	Asp Val Ala Tyr Leu Arg Ala	Leu Ser Leu Glu Val				
	450		455		460	
Ala Glu Glu Ile	Ala Arg Leu Glu Ala Glu Val	Phe Arg Leu Ala Gly				
	465		470		475	
His Pro Phe Asn	Leu Asn Ser Arg Asp	Gln Leu Glu Arg Val Leu Phe				
	485		490		495	
Asp Glu Leu Gly	Leu Pro Ala Ile Gly Lys Thr	Gln Lys Thr Gly Lys				
	500		505		510	
Arg Ser Thr Ser	Ala Ala Val Leu Glu Ala Leu Arg	Glu Ala His Pro				
	515		520		525	
Ile Val Glu Lys	Ile Leu Gln Tyr Arg Glu Leu Thr	Lys Leu Lys Ser				
	530		535		540	
Thr Tyr Ile Asp	Pro Leu Pro Asp Leu Ile His	Pro Arg Thr Gly Arg				
	545		550		555	
Leu His Thr Arg	Phe Asn Gln Thr Ala Thr Ala Thr	Gly Arg Leu Ser				
	565		570		575	
Ser Ser Asp Pro	Asn Leu Gln Asn Ile Pro Val Ala Thr	Pro Leu Gly				
	580		585		590	
Gln Arg Ile Arg	Arg Ala Phe Ile Ala Glu Glu Gly	Trp Leu Leu Val				
	595		600		605	
Ala Leu Asp Tyr	Ser Gln Ile Glu Leu Arg Val Leu Ala His	Leu Ser				
	610		615		620	
Gly Asp Glu Asn	Leu Ile Arg Val Phe Gln Glu Gly	Arg Asp Ile His				
	625		630		635	
					640	

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
                     645                    650                    655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
                     660                    665                    670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
                     675                    680                    685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
                     690                    695                    700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
                     705                    710                    715                    720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
                     725                    730                    735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
                     740                    745                    750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
                     755                    760                    765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
                     770                    775                    780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
                     785                    790                    795                    800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
                     805                    810                    815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
                     820                    825                    830  
 Glu His His His His His His  
                     835

<210> 176

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 176

cagaacatcc ccgtcgccac cccgcttggg cag

33

<210> 177

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 177

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cgggcccgggc cccacagccg gaggactttc cccggcaact cgccctcatc 300  
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480  
 ggggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcac 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
 cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
 gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccatgctcct cgctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200  
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320  
 gtccctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
 cttcccgcga tcaagaagac gcaaaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
 gaggccctcc gcgaggcca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgacctcttg ccggacctca tccaccccag gacgggcccgc 1680  
 ctccacacc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacactct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920



acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggaccc cctgatgcgc 1980  
 cgggcgcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgccccagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 178

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 178

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55				60					
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	



Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His  
 835

<210> 179  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 179  
gggcttcccg ccatcaagaa gacggagaag acc

33

<210> 180  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 180  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacgag 240  
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccggcc ggcgacgacc ccatgtctct cgctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200

gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320  
 gtcttgggcc atatggaggc cacgggggtg cgcttgagc tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgccgcg ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
 cttcccgcca tcggcaagac gcaaaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560  
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgaccccttg ccggacctca tccacccag gacggggcgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcgggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagacc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 181  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 181  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys  
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 182  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 182  
ctagggcttc ccgcatcaa gaagacgcaa aagaccggc

39

<210> 183  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 183  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggc cgagacggag gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480



ggggtaccta tcaccccgcc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgccc accgacctgc ccctggaggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
 ccccgccggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200  
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320  
 gtccctggccc atatggaggc cacgggggtg cgcttgagc tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgcccgc ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc cggggaccag ctggaaaggg tcctctttga cgagctaggg 1500  
 cttcccgcca tcggcaagac gaaaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560  
 gaggcctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680  
 ctccacacc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgtcggccca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagacc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340

ctccttcagg tcgccaacga gctgggtctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 184  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 184  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Glu Thr Glu Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu



Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 185

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 185

ccggggaaag tcctcctccg tctcggcccg gcccgctt



gagggcctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacggggccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggcg ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggaccc cctgatgcgc 1980  
cgggcgccca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 187

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 187

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105						110	



004250 4002450

Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
450						455					460				
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly
465					470					475					480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
			485						490					495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Gln	Lys	Thr	Gly	Lys
			500					505					510		
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro
		515					520					525			
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser
	530					535					540				
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg
545					550					555					560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser
				565					570					575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly
			580					585					590		
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val
		595					600					605			
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser
	610					615					620				
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His
625					630					635					640
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp
				645					650					655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr
			660					665					670		
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu
		675					680					685			
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val
	690					695					700				
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr
705					710					715					720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala
				725					730					735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
			740					745					750		
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
		755					760					765			
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
	770					775					780				



Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 188  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 188  
cgggacctcg aggcgcgtga accccaggag gtccac 36

<210> 189  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 189  
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caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcttacggg 240  
gggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc cctggagggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggcctt agggcctttc tggagaggct tgagtttggc 840

agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900  
 ccccgccggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960  
 gatcttcttg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
 aaagccctca gggacctgaa ggaggcgcg gggtcttctcg ccaaagacct gagcgttctg 1080  
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcccgcc gctacggcgg ggagtggacg 1200  
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
 cttgaggggg aggagaggct ctttggctt taccgggagg tggagaggcc cttttccgct 1320  
 gtccctggccc atatggaggg cacgggggtg cgcctggacg tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgccgcg ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500  
 cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccaccagcgc cgccgtcctg 1560  
 gaggcctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgacccttg ccggacctca tccacccag gacgggcccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctcaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc cccgggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcttg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340  
 ctccctcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gccgggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 190  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 190

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala

305		310		315		320
Asp Leu Leu Ala	Leu Ala Ala Ala Arg	Gly Gly Arg Val His Arg Ala				
	325		330		335	
Pro Glu Pro Tyr	Lys Ala Leu Arg Asp	Leu Lys Glu Ala Arg Gly Leu				
	340		345		350	
Leu Ala Lys Asp	Leu Ser Val Leu Ala Leu Arg	Glu Gly Leu Gly Leu				
	355		360		365	
Pro Pro Gly Asp	Asp Pro Met Leu Leu Ala Tyr	Leu Leu Asp Pro Ser				
	370		375		380	
Asn Thr Thr Pro	Glu Gly Val Ala Arg Arg Tyr	Gly Gly Glu Trp Thr				
	385		390		395	
Glu Glu Ala Gly	Glu Arg Ala Ala Leu Ser	Glu Arg Leu Phe Ala Asn				
	405		410		415	
Leu Leu Lys Arg	Leu Glu Gly Glu Glu Arg	Leu Leu Trp Leu Tyr Arg				
	420		425		430	
Glu Val Glu Arg	Pro Leu Ser Ala Val Leu Ala His	Met Glu Ala Thr				
	435		440		445	
Gly Val Arg Leu	Asp Val Ala Tyr Leu Arg Ala	Leu Ser Leu Glu Val				
	450		455		460	
Ala Glu Glu Ile	Ala Arg Leu Glu Ala Glu Val	Phe Arg Leu Ala Gly				
	465		470		475	
His Pro Phe Asn	Leu Asn Ser Arg Asp Gln	Leu Glu Arg Val Leu Phe				
	485		490		495	
Asp Glu Leu Arg	Leu Pro Lys Leu Lys Lys Thr	Lys Lys Thr Gly Lys				
	500		505		510	
Arg Ser Thr Ser	Ala Ala Val Leu Glu Ala Leu Arg	Glu Ala His Pro				
	515		520		525	
Ile Val Glu Lys	Ile Leu Gln Tyr Arg Glu Leu Thr	Lys Leu Lys Ser				
	530		535		540	
Thr Tyr Ile Asp	Pro Leu Pro Asp Leu Ile His	Pro Arg Thr Gly Arg				
	545		550		555	
Leu His Thr Arg	Phe Asn Gln Thr Ala Thr Ala Thr	Gly Arg Leu Ser				
	565		570		575	
Ser Ser Asp Pro	Asn Leu Gln Asn Ile Pro Val Arg Thr	Pro Leu Gly				
	580		585		590	
Gln Arg Ile Arg	Arg Ala Phe Ile Ala Glu Glu Gly Trp	Leu Leu Val				
	595		600		605	
Ala Leu Asp Tyr	Ser Gln Ile Glu Leu Arg Val Leu Ala His	Leu Ser				
	610		615		620	
Gly Asp Glu Asn	Leu Ile Arg Val Phe Gln Glu Gly Arg Asp	Ile His				
	625		630		635	
					640	

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
                     645                    650                    655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
                     660                    665                    670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
                     675                    680                    685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
                     690                    695                    700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
                     705                    710                    715                    720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
                     725                    730                    735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
                     740                    745                    750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
                     755                    760                    765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
                     770                    775                    780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
                     785                    790                    795                    800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
                     805                    810                    815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
                     820                    825                    830  
 Glu His His His His His His  
                     835

<210> 191

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 191

ctcctccacg agttcggc

18

<210> 192

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 192

accggtcttc ttcgtcttct tcaacttggg aagcctgagc tcgtcaaa

48

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1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

<400> 193  
aagacgaaga agaccggtaa gcgctccacc agc 33

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 194  
gtcgactcta gatcagtggt ggtgggtggtg gtgcttggcc gcccggcgca tc 52

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<220>
<221> modified_base
<222> (19)..(42)
<223> The bases in these positions within this primer
are 91% of the base shown and 3% each of the other
3 nucleotides.
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<400> 195  
ggagcgctta ccggtctttt gcgtcttctt gatcttggga agccttagct cgtcaaagag 60

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 196  
ctcctccacg agttcggc 18

<220>

<221> modified\_base  
 <222> (19)..(42)  
 <223> The bases at these positions within this primer  
 are 91% of the base shown and 3% each of the other  
 3 nucleotides.

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 197  
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<210> 198  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 198  
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<210> 199  
 <211> 2517  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 199  
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 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cgggcccggc cccacgcgcg gaggactttc cccggcaact cgcctcctc 300  
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccagctcct ccaccccgag 480  
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcctc 600  
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 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
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cgggcggcca	agaccatcaa	cttcgggggtc	ctctacggca	tgtcggccca	ccgcctctcc	2040
caggagctag	ccatccctta	cgaggaggcc	caggccttca	ttgagcgcta	ctttcagagc	2100
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gcccggctgg	ccaaggagg	catggagggg	gtgtatcccc	tggccgtgcc	cctggagggtg	2460
gaggtgggga	taggggagga	ctggctctcc	gccaaaggag	accaccacca	ccaccac	2517

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<210> 200
<211> 839
<212> PRT
<213> Artificial Sequence
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$\langle 400 \rangle$  200

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Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala



Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
                     645                    650                    655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
                     660                    665                    670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
                     675                    680                    685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
                     690                    695                    700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
                     705                    710                    715                    720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
                     725                    730                    735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
                     740                    745                    750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
                     755                    760                    765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
                     770                    775                    780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
                     785                    790                    795                    800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
                     805                    810                    815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
                     820                    825                    830  
 Glu His His His His His His  
                     835

<210> 201

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 201

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 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
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 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcg accgacctgc ccctggagggt ggacttcgcc 780  
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 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
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 ttcccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
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 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280

ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tcgccaacga gctggtcctc gaggcccca aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
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<210> 202  
<211> 839  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 202  
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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys	Leu	Ser	Trp	Asp 245	Leu	Ala	Lys	Val	Arg 250	Thr	Asp	Leu	Pro	Leu	Glu
Val	Asp	Phe	Ala 260	Lys	Arg	Arg	Glu	Pro 265	Asp	Arg	Glu	Arg	Leu 270	Arg	Ala
Phe	Leu	Glu 275	Arg	Leu	Glu	Phe	Gly 280	Ser	Leu	Leu	His	Glu 285	Phe	Gly	Leu
Leu	Glu 290	Ser	Pro	Lys	Ala	Leu 295	Glu	Glu	Ala	Pro	Trp 300	Pro	Pro	Pro	Glu
Gly 305	Ala	Phe	Val	Gly	Phe 310	Val	Leu	Ser	Arg	Lys 315	Glu	Pro	Met	Trp	Ala 320
Asp	Leu	Leu	Ala	Leu 325	Ala	Ala	Ala	Arg	Gly 330	Gly	Arg	Val	His	Arg 335	Ala
Pro	Glu	Pro	Tyr 340	Lys	Ala	Leu	Arg	Asp 345	Leu	Lys	Glu	Ala	Arg 350	Gly	Leu
Leu	Ala	Lys 355	Asp	Leu	Ser	Val	Leu 360	Ala	Leu	Arg	Glu	Gly 365	Leu	Gly	Leu
Pro	Pro 370	Gly	Asp	Asp	Pro	Met 375	Leu	Leu	Ala	Tyr	Leu 380	Leu	Asp	Pro	Ser
Asn 385	Thr	Thr	Pro	Glu	Gly 390	Val	Ala	Arg	Arg	Tyr 395	Gly	Gly	Glu	Trp	Thr 400
Glu	Glu	Ala	Gly	Glu 405	Arg	Ala	Ala	Leu	Ser 410	Glu	Arg	Leu	Phe	Ala	Asn
Leu	Leu	Lys	Arg 420	Leu	Glu	Gly	Glu	Glu 425	Arg	Leu	Leu	Trp	Leu 430	Tyr	Arg
Glu	Val	Glu 435	Arg	Pro	Leu	Ser	Ala 440	Val	Leu	Ala	His	Met 445	Glu	Ala	Thr
Gly	Val 450	Arg	Leu	Asp	Val	Ala 455	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
Ala 465	Glu	Glu	Ile	Ala	Arg 470	Leu	Glu	Ala	Glu	Val 475	Phe	Arg	Leu	Ala	Gly 480
His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp	Gln 490	Leu	Glu	Arg	Val	Leu 495	Phe
Asp	Glu	Leu	Arg 500	Ile	Pro	Lys	Ile	Lys 505	Lys	Thr	His	Lys	Thr 510	Gly	Lys
Arg	Ser	Thr 515	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu 525	Ala	His	Pro
Ile 530	Val	Glu	Lys	Ile	Leu	Gln 535	Tyr	Arg	Glu	Leu	Thr 540	Lys	Leu	Lys	Ser
Thr 545	Tyr	Ile	Asp	Pro	Leu 550	Pro	Asp	Leu	Ile	His 555	Pro	Arg	Thr	Gly	Arg 560
Leu	His	Thr	Arg	Phe 565	Asn	Gln	Thr	Ala	Thr 570	Ala	Thr	Gly	Arg	Leu 575	Ser

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 203  
 <211> 2517  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 203  
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc ggtgctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggg cccacacgcc gaggactttc cccggcaact cgcctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480  
gggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc ctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggagggt ggacttcgcc 780  
aaaaggcggg agcccagccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accggggccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctccgccc ggcgacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcccgcc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380  
tccttgaggg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500  
cttcccaagt tgaagaagac gaagaagacc ggtaagcgt ccagcagcgc cgccgtcctg 1560  
gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgacccttg ccggacctca tccacccag gacggggcgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920



acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcgggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
 caggagctag ccattccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tcgccaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 204

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 204

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105						110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135						140			
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170						175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510



<210> 205  
 <211> 2517  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 205  
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cgggcccggc cccacgccc gaggactttc cccggcaact cgccctcatc 300  
 aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480  
 gggtagctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatcccg gagaagatcc tggcccacat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgctc accgacctgc ccctggagggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
 cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgtcctt cgcctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200  
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320  
 gtccctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500  
 cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccaccagcgc cgccctcctg 1560





Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	
450						455					460					
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	
465					470					475					480	
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
			485						490					495		
Asp	Glu	Leu	Arg	Leu	Pro	Lys	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	
			500					505					510			
Arg	Ser	Thr	Ser	Ala	Ala	Leu	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	
		515					520					525				
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	
	530					535					540					
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	
545					550					555					560	
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565					570					575		
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	
			580					585					590			
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	
		595					600					605				
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	
	610					615					620					
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	
625					630					635				640		
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	
				645					650					655		
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	
			660					665					670			
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	
		675					680					685				
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	
	690					695					700					
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	
705					710					715				720		
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	
				725					730					735		
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	
			740					745					750			
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	
		755					760					765				
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	
	770					775					780					

0042304-0022300

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 207  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 207  
gtcggagggg tccccacga g 21

<210> 208  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 208  
tgtggaattg tgagcgg 17

<210> 209  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> modified\_base  
<222> (28)..(59)  
<223> The bases in these positions within this primer  
are 91% of the base shown and 3% each of the other  
3 nucleotides.

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 209  
ctcgtggggg acccctccga caacctcccc ggggtcaagg gcatcgggga gaagaccgcc 60  
ctcaagcttc tcaag 75

<210> 210  
<211> 23  
<212> DNA  
<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence: Synthetic

<400> 210

gtggcctcca tatgggccag gac

23

<210> 211

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 211

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcog ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccagag acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaccgccc tcgagggtccc cggtacgag 360  
gcgagcgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420  
atcctcaccg ccgaccgcca cctctaccaa ctctgtctcc accgcgtcgc cgtcctccac 480  
cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccg aggggtcagg 600  
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cggtgcgca ccgacctccc cctggagggtg 780  
gacctcgccc aggggcgggg gcccgaccgg gaggggctta gggccttcct ggagagggtg 840  
gagttcgga gcctcctcca cgagttcggc ctctggagg ccccgcccc cctggaggag 900  
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960  
atgtgggcgg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca 1020  
gacccttggt cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080  
gccgtcttgg cctcgaggga ggggctagac ctctgtcccc gggacgacct catgtcctc 1140  
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg 1200  
gagtggacgg aggacgccc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260  
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320  
ctctccccgg tcctggccca tatggaggcc accgggggtac ggcgggacgt ggctacctt 1380

caggcccttt ccctggagct tgcggaggag atccgccgcc tgcaggagga ggtcttccgc 1440  
 ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac 1500  
 gagcttaggc ttcccgctt gggaagacg caaaagacag gcaagcgctc caccagcgcc 1560  
 gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620  
 gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg 1680  
 acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740  
 tccgaccca acctgcagaa catccccgtc cgcacccct tgggccagag gatccgccgg 1800  
 gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860  
 cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920  
 gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980  
 ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040  
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100  
 ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacggccgg 2220  
 gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280  
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
 gcccgcacgc tcctccaggt cgccaacgag ctctcctgg agggcccccag agcgcgggcc 2400  
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
 ctggaggtgg aggtggggat gggggaggac tggtttccg ccaagggtca ccaccaccac 2520  
 caccac 2526

<210> 212

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 212

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60

Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Arg	Gly	Val	Arg	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	245	250	255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val	325	330	335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	340	345	350	
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	355	360	365	
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	370	375	380	
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	385	390	395	400

0057304-000000

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys  
500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
                     740                    745                    750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
                     755                    760                    765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
                     770                    775                    780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
                     785                    790                    795                    800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
                     805                    810                    815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
                     820                    825                    830  
 Ser Ala Lys Gly His His His His His His  
                     835                    840

<210> 213  
 <211> 2526  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 213  
 atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
 gaaccggtgc aggcgttcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
 gggtagaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttccg ccacgaggcc 240  
 tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc 300  
 ctcatcaagg agctggtgga cctcctggggg ttaccgccg tcgaggtccc cggctacgag 360  
 gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420  
 atcctcaccg ccgaccgcga cctctaccaa ctctctccg accgcgtcgc cgtcctccac 480  
 cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
 cagtgggtgg acttccgcgc cctcgtgggg gacctctccg acaacctccc cggggtcaag 600  
 ggcatcgggg agtataccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
 ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
 gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
 gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttctt ggagaggctg 840  
 gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900  
 gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc 960



<400> 214

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15  
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30  
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45  
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60  
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80  
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125  
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Tyr Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240  
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255  
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
260 265 270  
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
275 280 285  
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val

004360 4062650

325										330					335				
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val				
		340						345					350						
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly				
		355					360					365							
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu				
	370					375					380								
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly				
	385				390					395				400					
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu				
			405					410						415					
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp				
		420					425					430							
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met				
	435						440					445							
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser				
	450					455					460								
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg				
	465				470					475				480					
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg				
			485					490					495						
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys				
		500						505					510						
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu				
		515					520					525							
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys				
	530					535				540									
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg				
	545				550					555				560					
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly				
			565					570						575					
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr				
		580						585					590						
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp				
		595					600					605							
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala				
	610					615					620								
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys				
	625				630				635					640					
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu				
			645						650					655					



Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 215  
<211> 2526  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 215  
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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg cgtcttcgt ggtctttgac gccaaagccc cctccttcg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccagg acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgaggtccc cggctacgag 360  
gcggacgacg ttctcgccac cctggccaag aaggcgaaa aggaggggta cgaggtgcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480

11729, 11730, 11731, 11732, 11733, 11734, 11735, 11736, 11737, 11738, 11739, 11740, 11741, 11742, 11743, 11744, 11745, 11746, 11747, 11748, 11749, 11750, 11751, 11752, 11753, 11754, 11755, 11756, 11757, 11758, 11759, 11760, 11761, 11762, 11763, 11764, 11765, 11766, 11767, 11768, 11769, 11770, 11771, 11772, 11773, 11774, 11775, 11776, 11777, 11778, 11779, 11780, 11781, 11782, 11783, 11784, 11785, 11786, 11787, 11788, 11789, 11790, 11791, 11792, 11793, 11794, 11795, 11796, 11797, 11798, 11799, 11800, 11801, 11802, 11803, 11804, 11805, 11806, 11807, 11808, 11809, 11810, 11811, 11812, 11813, 11814, 11815, 11816, 11817, 11818, 11819, 11820, 11821, 11822, 11823, 11824, 11825, 11826, 11827, 11828, 11829, 11830, 11831, 11832, 11833, 11834, 11835, 11836, 11837, 11838, 11839, 11840, 11841, 11842, 11843, 11844, 11845, 11846, 11847, 11848, 11849, 11850, 11851, 11852, 11853, 11854, 11855, 11856, 11857, 11858, 11859, 11860, 11861, 11862, 11863, 11864, 11865, 11866, 11867, 11868, 11869, 11870, 11871, 11872, 11873, 11874, 11875, 11876, 11877, 11878, 11879, 11880, 11881, 11882, 11883, 11884, 11885, 11886, 11887, 11888, 11889, 11890, 11891, 11892, 11893, 11894, 11895, 11896, 11897, 11898, 11899, 11900, 11901, 11902, 11903, 11904, 11905, 11906, 11907, 11908, 11909, 11910, 11911, 11912, 11913, 11914, 11915, 11916, 11917, 11918, 11919, 11920, 11921, 11922, 11923, 11924, 11925, 11926, 11927, 11928, 11929, 11930, 11931, 11932, 11933, 11934, 11935, 11936, 11937, 11938, 11939, 11940, 11941, 11942, 11943, 11944, 11945, 11946, 11947, 11948, 11949, 11950, 11951, 11952, 11953, 11954, 11955, 11956, 11957, 11958, 11959, 11960, 11961, 11962, 11963, 11964, 11965, 11966, 11967, 11968, 11969, 11970, 11971, 11972, 11973, 11974, 11975, 11976, 11977, 11978, 11979, 11980, 11981, 11982, 11983, 11984, 11985, 11986, 11987, 11988, 11989, 11990, 11991, 11992, 11993, 11994, 11995, 11996, 11997, 11998, 11999, 12000, 12001, 12002, 12003, 12004, 12005, 12006, 12007, 12008, 12009, 12010, 12011, 12012, 12013, 12014, 12015, 12016, 12017, 12018, 12019, 12020, 12021, 12022, 12023, 12024, 12025, 12026, 12027, 12028, 12029, 12030, 12031, 12032, 12033, 12034, 12035, 12036, 12037, 12038, 12039, 12040, 12041, 12042, 12043, 12044, 12045, 12046, 12047, 12048, 12049, 12050, 12051, 12052, 12053, 12054, 12055, 12056, 12057, 12058, 12059, 12060, 12061, 12062, 12063, 12064, 12065, 12066, 12067, 12068, 12069, 12070, 12071, 12072, 12073, 12074, 12075, 12076, 12077, 12078, 12079, 12080, 12081, 12082, 12083, 12084, 12085, 12086, 12087, 12088, 12089, 12090, 12091, 12092, 12093, 12094, 12095, 12096, 12097, 12098, 12099, 12100, 12101, 12102, 12103, 12104, 12105, 12106, 12107, 12108, 12109, 12110, 12111, 12112, 12113, 12114, 12115, 12116, 12117, 12118, 12119, 12120, 12121, 12122, 12123, 12124, 12125, 12126, 12127, 12128, 12129, 12130, 12131, 12132, 12133, 12134, 12135, 12136, 12137, 12138, 12139, 12140, 12141, 12142, 12143, 12144, 12145, 12146, 12147, 12148, 12149, 12150, 12151, 12152, 12153, 12154, 12155, 12156, 12157, 12158, 12159, 12160, 12161, 12162, 12163, 12164, 12165, 12166, 12167, 12168, 12169, 12170, 12171, 12172, 12173, 12174, 12175, 12176, 12177, 12178, 12179, 12180, 12181, 12182, 12183, 12184, 12185, 12186, 12187, 12188, 12189, 12190, 12191, 12192, 12193, 12194, 12195, 12196, 12197, 12198, 12199, 12200, 12201, 12202, 12203, 12204, 12205, 12206, 12207, 12208, 12209, 12210, 12211, 12212, 12213, 12214, 12215, 12216, 12217, 12218, 12219, 12220, 12221, 12222, 12223, 12224, 12225, 12226, 12227, 12228, 12229, 12230, 12231, 12232, 12233, 12234, 12235, 12236, 12237, 12238, 12239, 12240, 12241, 12242, 12243, 12244, 12245, 12246, 12247, 12248, 12249, 12250, 12251, 12252, 12253, 12254, 12255, 12256, 12257, 12258, 12259, 12260, 12261, 12262, 12263, 12264, 12265, 12266, 12267, 12268, 12269, 12270, 12271, 12272, 12273, 12274, 12275, 12276, 12277, 12278, 12279, 12280, 12281, 12282, 12283, 12284, 12285, 12286, 12287, 12288, 12289, 12290, 12291, 12292, 12293, 12294, 12295, 12296, 12297, 12298, 12299, 12300, 12301, 12302, 12303, 12304, 12305, 12306, 12307, 12308, 12309, 12310, 12311, 12312, 123

gccccgatgc tcctccaggt cgccaacgag ctctctctgg aggcccccca agcgcggggcc 2400  
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520  
caccac 2526

<210> 216  
<211> 842  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 216  
Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15  
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30  
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45  
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60  
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80  
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125  
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Arg Glu Lys Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240



Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
                   580                  585                  590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
                   595                  600                  605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
                   610                  615                  620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
                   625                  630                  635                  640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
                   645                  650                  655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
                   660                  665                  670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
                   675                  680                  685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
                   690                  695                  700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
                   705                  710                  715                  720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
                   725                  730                  735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
                   740                  745                  750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
                   755                  760                  765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
                   770                  775                  780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
                   785                  790                  795                  800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
                   805                  810                  815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
                   820                  825                  830  
 Ser Ala Lys Gly His His His His His His  
                   835                  840

<210> 217

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 217

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cggggccgggc cccacgcccg gaggactttc cccggcaact cgccctcatc 300  
 aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480  
 ggggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
 aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtctggc 840  
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
 aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccattgctcct cgctacctc 1140  
 ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200  
 gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320  
 gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380  
 tccctggagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500  
 cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560  
 gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgaccttgg ccggacctca tccaccccag gacgggcccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctccaga acatccccgt ccgcacccg cttgggcaga ggatccgccg ggcttcatc 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggag ggacatccac 1920

# 2025

<211> 839

<212> PRT

<220>

<400> 218

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510



Arg Ser Ser Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His  
 835

<210> 219  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 219  
cgggacctcg aggcgcgtga accccaggag gtccac 36

<210> 220  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 220  
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cgagacggag gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgctc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgtctct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200

gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380  
tccctggagg tggccgagga gatcgcccg ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500  
cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560  
gaggccctcc gcgaggccca ccccatcgctg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacggggccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggag ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
cgggcgccca agaccatcaa ctctgggggtc ctctacggca tgtcgggcca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tcgccaacga gctggtcctc gaggccccaa aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 221  
<211> 839  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 221  
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45



Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr		
385					390					395					400		
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn		
				405					410					415			
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg		
			420					425					430				
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr		
			435				440					445					
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val		
	450					455					460						
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly		
465					470					475					480		
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe		
			485						490					495			
Asp	Glu	Leu	Arg	Leu	Pro	Lys	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys		
			500					505					510				
Arg	Ser	Ser	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro		
			515				520					525					
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser		
	530					535					540						
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg		
545					550					555					560		
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser		
				565					570					575			
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly		
			580					585					590				
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val		
		595					600					605					
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser		
	610					615					620						
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His		
625					630					635				640			
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp		
				645					650					655			
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr		
			660					665					670				
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu		
		675					680					685					
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val		
	690					695					700						
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr		
705					710					715					720		

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His  
835

<210> 222  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 222  
ccggggaaag tcctcctccg tctcggcccg gccgcctt 39

<210> 223  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 223  
gtcggactcg tcaccggtca gggc 24

<210> 224  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> modified\_base  
<222> (28)..(60)  
<223> The bases in these positions within this primer  
are 91% of the base shown and 3% each of the other  
3 nucleotides.

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 224

ctgaccggtg acgagtcga caaccttccc ggggtcaagg gcatcgggga gaggacggcg 60

aggaagcttc tggag

75

<210> 225

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 225

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120

ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240

gggtacaagg cgggccgggc cccacgccc gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480

gggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caatggcatc 600

ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660

aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720

aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840

agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900

cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggac 960

gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020

aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080

gccctgaggg aaggccttgg cctcccgcc ggcgacgacc ccattgctcct cgcctacctc 1140

ctggaccctt cgaacaccac ccccagggg gtggcccgcc gctacggcgg ggagtggacg 1200

gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260

cttgaggggg aggagaggct cttttggctt taccgggagg tggagaggcc cttttccgct 1320

gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380

tccctggagg tggccgagga gatcgcccgc ctcgaggccg aggtcttccg cctggccggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500  
 cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560  
 gagggcctcc gcgaggccca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
 aagctgaaga gcacctacat tgaccccttg ccggacctca tccacccag gacgggcccgc 1680  
 ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
 aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800  
 gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
 gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920  
 acggagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggacc cctgatgcgc 1980  
 cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
 ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
 gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
 gtgccccagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
 ctcttcagg tcgccaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400  
 gcccggtg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 226

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 226

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75				80	







Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His His  
835

<210> 227

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 227

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag 120  
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggc cccacgcccg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccgcc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cgcagaggaa gcttctggag gagggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
aagctctcct gggacctggc caaggtgccc accgacctgc ccctggagggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
agcctcctcc acgagttcgg cttcttgaa agcccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020

aaagccctca gggacctgaa ggaggcgcg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cttttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgcttgacg tggcctatct cagggccttg 1380  
tccctggagg tggccgagga gatcgcccgc ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500  
cttcccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560  
gaggccctcc gcgaggccca ccccatcgct gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgacccttg ccggacctca tccaccccag gacgggcccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccc ggcttcatc 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct caggggtgctg 1860  
gccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggggc ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980  
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160  
gtggagaccc tcttcggccg ccgccgctac gtgccagacc tagaggcccg ggtgaagagc 2220  
gtgcgaggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
ctcatgaagc tggctatggt gaagctcttc cccaggctgg aggaaatggg ggccaggatg 2340  
ctccttcagg tcgccaacga gctggtcctc gaggcccaa aagagagggc ggaggccgtg 2400  
gcccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg 2460  
gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 228

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 228

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5				10						15	

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Gln Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Ser Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 229

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 229

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60  
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cggcctcatc 300  
 aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
 gggtagctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatg 600  
 ggggagaaga cggggaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660





<210> 230  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 230

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Met	Gly	Glu	Lys	Thr	Gly	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
	225				230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			



Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His His  
 835

<210> 231  
 <211> 2517  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 231  
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctct ggtggacggc 60  
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
 ccggtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 ggggtacaagg cgggccgggc ccccaagccg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggttcacg cgctcagagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcacccctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggccttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcacg 600  
ggggagaata cggcgaggaa gcttctggag gagggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caagggtgcg accgacctgc ccctggagggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagagggt tgagtttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcccc cgagccttat 1020  
aaagccctca gggacctgaa ggaggcgcg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctccccgcc ggcgacgacc ccatgctcct cgctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcccgcc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gcttaagagg 1260  
cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgctggacg tggcctatct cagggccttg 1380  
tccttgagg tggccgagga gatcgccgc ctcgaggccg aggtcttccg cctggccggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tcctctttga cgagctcagg 1500  
cttccaagt tgaagaagac gaagaagacc ggtaagcgct ccagcagcgc cgccgtcctg 1560  
gaggccctcc gcgaggcca ccccatcgtg gagaagatcc tgcagtaccg ggagctcacc 1620  
aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacgggcccgc 1680  
ctccacacc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740  
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggcccttcac 1800  
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860  
gccacctct ccggcgacga gaacctgate cgggtcttcc aggaggggcg ggacatccac 1920  
acggagaccg ccagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980  
cgggcggcca agaccatcaa cttcgggggtc ctctacggca tgcgggcca ccgcctctcc 2040  
caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100  
ttccccaagg tgcgggcctg gattgagaag accctggagg agggcaggag gcgggggtac 2160



210					215					220					
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
		290					295				300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
			325						330					335	
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu
			340					345					350		
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu
		355					360					365			
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
		370				375					380				
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr
385					390					395					400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn
			405						410					415	
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg
			420				425						430		
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr
		435					440					445			
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val
		450				455					460				
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly
465					470					475					480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
			485						490					495	
Asp	Glu	Leu	Arg	Leu	Pro	Lys	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys
			500					505					510		
Arg	Ser	Ser	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro
		515					520					525			
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser
		530				535					540				

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Glu His His His His His  
 835

<210> 233  
 <211> 2517  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 233

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ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccgggc cccacgcccg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360  
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gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaagc cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcmc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
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ctggaccctt cgaacaccac ccccagggg gtggcccggc gctacggcgg ggagtggacg 1200  
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 ctcttccagg tcgccaacga gctggctctc gaggcccaa aagagagggc ggaggccctg 2400  
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggagggtg 2460  
 gaggtgggga taggggagga ctggctctcc gccaaaggagc accaccacca ccaccac 2517

<210> 234

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 234

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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
						135					140				





Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu His His His His His  
835

<210> 235  
<211> 2517  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 235  
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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggc cccacgccc gaggaacttc cccggcaact cgcctcatc 300  
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccgcc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720  
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aaaaggcggg agcccagccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
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ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960  
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cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320  
gtcctggccc atatggaggc cacgggggtg cgcctggacg tggcctatct cagggccttg 1380



Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
		180						185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
	195						200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265						270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala
305					310					315					320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala
			325						330					335	
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu
			340					345						350	
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu
		355					360					365			
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser
	370					375					380				
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr
385					390					395					400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn
				405					410					415	

0057304 00400

Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	
			420					425					430			
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
		435					440					445				
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	
	450					455					460					
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	
465					470					475					480	
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
			485						490					495		
Asp	Glu	Leu	Arg	Leu	Pro	Lys	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	
			500					505					510			
Arg	Ser	Ser	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	
		515					520					525				
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	
	530					535					540					
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	
545					550					555					560	
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565					570					575		
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	
			580					585					590			
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	
		595					600					605				
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	
	610					615					620					
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	
625					630					635				640		
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	
				645					650					655		
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	
			660					665					670			
Gly	Met	Ser	Ala	His	Ala	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	
		675					680					685				
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	
	690					695					700					
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	
705					710					715					720	
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	
				725					730					735		
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	
			740					745					750			





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<210> 239  
 <211> 839  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 239

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
			35				40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
	65				70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
	225				230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265						270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540  
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800  
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Gly His His His His His His  
 835

<210> 240  
 <211> 2526  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 240  
 atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
 gggtagaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240  
 tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300

ctcatcaagg agctggtgga cctcctgggg tttacccgcc tctgaggtccc cggctacgag 360  
gcggaacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctctgtctccg accgcgtcgc cgtcctccac 480  
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag 600  
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg 780  
gacctcggcc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840  
gagttcggca gcctcctcca cgagttcggc ctctggagg ccccgcccc cctggaggag 900  
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctcccc ccccgagccc 960  
atgtgggagg agcttaaagc cctggccgcc tgcaggggag gccgcgtcca cggggcccc 1020  
gagccttata aagccctcag ggacctgaag gaggcgcggg ggcttctcgc caaagacctg 1080  
agcgttcttg ccctgagggg aggccttggc ctcccccccc gcgacgacct catgctctc 1140  
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcccggcg ctacggcggg 1200  
gagtggacgg aggagggggg ggagcgggccc gccctttccg agaggctctt cgccaacctg 1260  
cttaagaggc ttgaggggga ggagaggctc ctttggcttt accgggaggt ggagaggccc 1320  
ctttccgctg tcttggccca tatggaggcc acgggggtgc gcctggacgt ggcctatctc 1380  
agggccttgt ccctggaggt ggccgaggag atcgcccgcc tctgaggcca ggtcttccgc 1440  
ctggccggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt cctctttgac 1500  
gagctagggc ttcccgccat caagaagacg caaaagaccg gcaagcgctc caccagcgcc 1560  
gccgtcctgg agggcctccg cgaggcccac cccatcgtgg agaagatcct gcagtaccgg 1620  
gagctacca agctgaagag cacctacatt gaccccttgc cggacctcat ccaccccagg 1680  
acgggcccgc tccacaccg cttcaaccag acggccacgg ccacgggcag gctaagtagc 1740  
tccgatccca acctccagaa catccccgtc cgcacccccg ttgggcagag gatccgcccg 1800  
gccttcatcg ccgaggaggg gtggctattg gtggccctgg actatagcca gatagagctc 1860  
aggggtgctg cccacctctc cggcgacgag aacctgatcc gggcttcca ggagggggcg 1920  
gacatccaca cggagaccgc cagctggatg ttcggcgctc cccgggaggc cgtggacccc 1980  
ctgatgcgcc gggcgggcaa gaccatcaac ttcgggggtc tctacggcat gtcggccac 2040  
cgctctccc aggagctagc catcccttac gaggagggcc aggccttcat tgagcgctac 2100  
tttcagagct tccccaaagg gcgggcctgg attgagaaga ccctggagga gggcaggagg 2160

cgggggtacg tggagaccct cttcgggccgc cgccgctacg tgccagacct agaggcccg 2220  
 gtgaagagcg tgcgggagggc ggccgagcgc atggccttca acatgcccgt ccagggcacc 2280  
 gccgccgacc tcatgaagct ggctatggtg aagctcttcc ccaggctgga ggaaatgggg 2340  
 gccaggatgc tccttcaggt cgccaacgag ctggctctcg aggcccaaaa agagagggcg 2400  
 gagggcgtgg cccggctggc caaggaggtc atggaggggg tgtatcccct ggccgtgccc 2460  
 ctggaggtgg aggtggggat aggggaggac tggctctccg ccaaggagca ccaccaccac 2520  
 caccac 2526

<210> 241  
 <211> 842  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 241  
 Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
 1 5 10 15  
 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30  
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45  
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60  
 Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80  
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 85 90 95  
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110  
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125  
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140  
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly  
 355 360 365  
 Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu  
 405 410 415  
 Phe Ala Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp  
 420 425 430  
 Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser  
 450 455 460  
 Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp  
 595 600 605  
 Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg  
 625 630 635 640  
 Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala  
 785 790 795 800  
 Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Glu His His His His His His  
 835 840

<210> 242  
 <211> 2508  
 <212> DNA  
 <213> Artificial Sequence



<220>

<223> Description of Artificial Sequence: Synthetic

<400> 242

atggaattca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac 60  
ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag 120  
ccggtgcaga tggcttacgg cttcgccccg agcctcctca aggccttgaa ggaggacgga 180  
caggcggtgg tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacgag 240  
gcctacaagg cgggcccggg cccacccccg gaggacttcc cccgccagct cgccttggtc 300  
aagcggctgg tggaccttct gggcctggtc cgcctcgagg ccccggggta cgaggcggac 360  
gacgtcctgg gcaccctggc caagaaggcc gaaagggagg ggatggaggt gcgcctcctc 420  
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac 480  
gggaccctgg tcaccccaaa ggacgtccag gagaagtacg gggtgcccc ggagcgctgg 540  
gtggacttcc gcgccctcac gggggaccgc tcggacaaca tccccggggt ggcggggata 600  
ggggagaaga ccgcccttcg actcctcgca gagtggggga gcgtggaaaa cctcctgaag 660  
aacctggacc gggtaaagcc ggactcgctc cggcgcaaga tagaggcgca cctcgaggac 720  
ctccacctct ccttagacct ggcccgcatc cgcaccgacc tccccctgga ggtggacttt 780  
aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg 840  
gagttcggaa gcctcctcca cgagttcggc ctctggggag gggagaagcc ccgggaggag 900  
gccccctggc ccccgccga aggggccttc gtgggcttcc tcctttcccg caaggagccc 960  
atgtgggcgg agcttctggc cctggcggcg gcctcgagg gccgggtcca ccgggcaaca 1020  
agcccgggtg aggcctggc cgacctcaag gagggccggg ggttcctggc caaggacctg 1080  
gccgttttgg ccctgcggga ggggggtggc ctggacccca cggacgacct cctcctggtg 1140  
gcctacctcc tggaccggc caacaccac cccgaggggg tggccggcg ctacgggggc 1200  
gagttcacgg aggacgcagc ggagagggcc ctctctccg agaggctctt ccagaacctc 1260  
tttaaacggc tttccgagaa gtcctctgg ctctaccagg aggtggagcg gccctctcc 1320  
cgggtcttgg ccacatgga gggccggggg gtgaggctgg acgtccccct tctggaggcc 1380  
ctctcctttg agctggagaa ggagatggag cgcctggagg gggaggtctt ccgtttggcc 1440  
ggccaccct tcaacctcaa ctcccgcgac cagctggaaa gggtcctctt tgacgagctg 1500  
ggcctacccc cgggtgggccc gacgcagaag acgggcaagc gctccaccgc ccagggggcc 1560  
ctggaggccc tccggggggc ccacccatc gtggagctca tcctccagta ccgggagctt 1620  
tccaagctca aaagcaccta cctggacccc ctgccccggc tcgtccacct gcggacgggc 1680  
cggctccaca cccgcttcaa ccagacggcc acggccacgg gaaggctttc cagctccgac 1740

cccaacctgc agaacatccc cgtgcgcacc cccttggggc agcgcacccg caaggccttc 1800  
 gtggccgagg aggggtggct ccttttggcg gcggactact cccagattga gctccgggtc 1860  
 ctggcccacc tctcggggga cgagaacctg aagcgggtct tccgggaggg gaaggacatc 1920  
 cataccgaga ccgccgcctg gatgttcggc ttagaccccg ctctggtgga tccaaagatg 1980  
 cgccggggcg ccaagacggt caacttcggc gtctctacg ggatgtccgc ccacaggctc 2040  
 tcccaggagc tcggcataga ctacaaggag gcggaggcct ttattgagcg ctacttccag 2100  
 agcttcccca aggtgcgggc ctggatagaa aggaccctgg aggagggccg gacgcggggc 2160  
 tacgtggaga ccctgttcgg caggaggcgc tatgtgcccg acctggcctc ccgggtccgc 2220  
 tcggtgcggg aggcggcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgcc 2280  
 gacctgatga agatcgccat ggtcaagctc ttccccaggc taaagcccct gggggcccac 2340  
 ctctctctcc aagtgcacaa cgagctggtc ctggagggtc ccgaggaccg ggccgaggag 2400  
 gccaaaggccc tgggtcaagga ggtcatggag aacgcctacc ccctggacgt gccctcgag 2460  
 gtggaggtgg gcgtgggtcg ggactggctg gaggcgaagc aggattga 2508

<210> 243  
 <211> 835  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 243  
 Met Glu Phe Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val  
 1 5 10 15  
 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu  
 20 25 30  
 Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe  
 35 40 45  
 Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
 65 70 75 80  
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu  
 100 105 110  
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg  
 130 135 140



Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Gln Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His  
 515 520 525  
 Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys  
 530 535 540  
 Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu  
 595 600 605  
 Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val  
 645 650 655  
 Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr  
 675 680 685  
 Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala  
 725 730 735  
 Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln  
 770 775 780  
 Val His Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu  
 785 790 795 800  
 Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp  
 805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala  
820 825 830

Lys Gln Asp  
835

<210> 244  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 244  
cttccagaac ctctttaaac ggctttccga gaag 34

<210> 245  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 245  
cttctcggaa agccgtttaa agaggttctg gaag 34

<210> 246  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 246  
ccggtgggcc ggacgcagaa gacgggcaag c 31

<210> 247  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 247  
gcttgcccgt cttctgcgtc cggcccaccg g 31

<210> 248  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 248  
ctcctccaag tgcacaacga gctggctcctg g

31

<210> 249  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 249  
ccaggaccag ctcgttgtgc acttggagga g

31

<210> 250  
<211> 2499  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 250  
atggaattcc tgcccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac 60  
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc 120  
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg 180  
gtgatcgtgg tgtttgacgc caaggccccc tccttccgcc accagaccta cgaggcctac 240  
aaggcggggc gggctccac ccccgaggac tttcccggc agcttgccct tatcaaggag 300  
atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc 360  
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcac cctcaccgcg 420  
gaccgggacc ttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac 480  
ctgatcacc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac 540  
taccgggcct tggccgggga cccttccgac aacatccccg gcgtgaaggg catcggggag 600  
aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg 660  
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag 720  
ctatccctgg agctatcccg ggtgcacacg gacttgctcc ttcaggtgga cttcgcccgg 780  
cgccgggagc cggaccggga ggggcttaag gcctttttgg agaggctgga gttcggaagc 840  
ctcctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg 900  
cccccgagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag 960  
cttaacgcct tggccgccgc ctgggagggga agggtttacc gggcggagga tcccttggag 1020  
gccttgcggg ggcttgggga ggtgaggggg cttttggcca aggacctggc ggtgctggcc 1080  
ctgaggggaag ggattgccct ggcaccgggc gacgaccca tgctcctcgc ctacctcctg 1140

gatccttcca acaccgcccc cgaaggggta gcccggcgct acggggggga gtggaccgag 1200  
gaggcggggg aaagggcgct gctttccgaa aggctttacg ccgccctcct gaagcggtt 1260  
aagggggagg agaggcttct ttggctttac gaggaggtgg aaaagcccct ttcgcgggtc 1320  
ctggcccaca tggaggccac ggggggtacg ttggatgtgg cctacttaaa ggccctttcc 1380  
ctggaggtgg aggcggagat aaggcgcttc gaggaggagg tccaccgcct ggccgggcat 1440  
cctttcaacc tgaactcccc ggaccagctg gaaagggta tctttgacga gcttgggctt 1500  
cccgccatcg gcaagacgca gaagacgggc aagcgctcca ccagcgccgc cgttttggag 1560  
gccttgcggg aggtcatcc catcgtggac cgcctccttc agtaccggga gctttccaag 1620  
ctcaagggaa cctacatcga tcccttgctt gccctggtcc accccaagac gaaccgcctc 1680  
cacaccgtt tcaaccagac ggccaccgcc acggggaggc ttagcagctc ggatcctaata 1740  
ctgcaaaata tccccgtgcg caccctttg ggccagcgga tccgcccggc cttcgtggcc 1800  
gaggaggggt ggaggctggt ggttttggac tacagccaga ttgagctcag ggtcctggcg 1860  
cacctttccg gggacgagaa cctaataccg gtcttccagg agggccagga catccacacc 1920  
cagacggcca gctggatgtt cggcggtgcc ccagaggccg tggattccct gatgcgccgg 1980  
gcggccaaaga ccatcaactt cggcgctcctc tacggcatgt ccgcccaccg gctttcgga 2040  
gagctggcca tcccctacga ggaggcggtg gccttcatcg agcggtatct ccagagctac 2100  
ccaaggtgc gggcctggat tgagaaaacc ctggcggaag gacgggaacg gggctatgtg 2160  
gaaaccctct ttggccgccc gcgctacgtg cccgacttgg cttcccgggt gaagagcatc 2220  
cgggaggcag cggagcgcat ggccttcaac atgccggtcc aggggaccgc cgcggatttg 2280  
atgaaactgg ccatggtgaa gctctttccc aggcttcagg agctgggggc caggatgctt 2340  
ttgcaggtgc acaacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtcgcc 2400  
caggaggcca agcggaccat ggaggaggtg tggcccctga aggtgccctt ggaggtggaa 2460  
gtgggcatcg gggaggactg gctttccgcc aaggcctag 2499

<210> 251

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 251

Met	Glu	Phe	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	

Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		

Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr
145					150					155					160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser
				165					170					175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
			180					185					190		
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg
		195					200					205			
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys
	210					215					220				
Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys
225					230					235					240
Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	Leu	Leu	Gln	Val
			245						250					255	
Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	Phe
			260					265					270		
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu
		275					280					285			
Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly
	290					295					300				
Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu
305					310					315					320
Leu	Asn	Ala	Leu	Ala	Ala	Ala	Trp	Glu	Gly	Arg	Val	Tyr	Arg	Ala	Glu
				325					330					335	
Asp	Pro	Leu	Glu	Ala	Leu	Arg	Gly	Leu	Gly	Glu	Val	Arg	Gly	Leu	Leu
			340					345					350		
Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Ile	Ala	Leu	Ala
		355					360					365			



Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	
	370					375					380					
Thr	Ala	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	
385					390					395					400	
Glu	Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	Tyr	Ala	Ala	Leu	
				405					410					415		
Leu	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	
			420					425					430			
Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	
		435					440					445				
Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Lys	Ala	Leu	Ser	Leu	Glu	Val	Glu	
	450					455					460					
Ala	Glu	Ile	Arg	Arg	Phe	Glu	Glu	Glu	Val	His	Arg	Leu	Ala	Gly	His	
465					470					475					480	
Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Ile	Phe	Asp	
				485					490					495		
Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Gln	Lys	Thr	Gly	Lys	Arg	
			500					505					510			
Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	
		515					520					525				
Val	Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Ser	Lys	Leu	Lys	Gly	Thr	
	530					535					540					
Tyr	Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Asn	Arg	Leu	
545					550					555					560	
His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	
				565				570						575		
Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	
			580					585					590			
Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Arg	Leu	Val	Val	
		595					600					605				
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	
	610					615					620					
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Gln	Asp	Ile	His	Thr	
625					630					635				640		
Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Ser	
				645					650					655		
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	
			660					665					670			
Met	Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	
		675					680					685				
Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	
	690					695					700					

Ala	Trp	Ile	Glu	Lys	Thr	Leu	Ala	Glu	Gly	Arg	Glu	Arg	Gly	Tyr	Val
705					710					715					720
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Ala	Ser	Arg
				725					730					735	
Val	Lys	Ser	Ile	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro
			740					745					750		
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
		755					760					765			
Phe	Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His
	770					775					780				
Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Gln	Ala	Glu	Glu	Val	Ala
785					790					795					800
Gln	Glu	Ala	Lys	Arg	Thr	Met	Glu	Glu	Val	Trp	Pro	Leu	Lys	Val	Pro
			805						810					815	
Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Ala
			820					825					830		

<210> 252  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 252  
 gccgccctcc tgaagcggct taaggg 26

<210> 253  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 253  
 cccttaagcc gcttcaggag ggcggc 26

<210> 254  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 254  
 atcggcaaga cgcagaagac gggcaagc 28

<210> 255  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 255  
gcttgcccgt cttctgcgtc ttgccgat 28

<210> 256  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 256  
ttgcagggtgc acaacgaact ggtcctc 27

<210> 257  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 257  
gaggaccagt tcgttgtgca cctgcaa 27

<210> 258  
<211> 2526  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 258  
atgaattcca cccactttt tgacctggag gaacccccca agcgggtgct tctggtggac 60  
ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag 120  
ccggtgcaga tgggtctacgg cttcgcccgg agcctcctca aggccttgaa ggaggacgga 180  
caggcgggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcttacgag 240  
gcctacaagg cgggcccggc cccacccccg gaggacttcc cccgccagct cgccttggtc 300  
aagcggctgg tggaccttct gggcctgggtc cgcctcgagg ccccggggta cgaggcggac 360  
gacgtcctgg gcacctggc caagaaggcc gaaagggagg ggatggaggt gcgcacctc 420  
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac 480



gccccgatgc tcctccaggt cgccaacgag ctctcctgg agggccccc agcgcgggcc 2400  
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520  
caccac 2526

<210> 259  
<211> 842  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 259  
Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val  
1 5 10 15  
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu  
20 25 30  
Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe  
35 40 45  
Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
65 70 75 80  
Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu  
100 105 110  
Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys  
115 120 125  
Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg  
130 135 140  
Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp  
145 150 155 160  
Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro  
165 170 175  
Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp  
180 185 190  
Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu  
195 200 205  
Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp  
225 230 235 240

Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
                     580                    585                    590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
                     595                    600                    605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
                     610                    615                    620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
                     625                    630                    635                    640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
                     645                    650                    655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
                     660                    665                    670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
                     675                    680                    685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
                     690                    695                    700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
                     705                    710                    715                    720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
                     725                    730                    735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
                     740                    745                    750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
                     755                    760                    765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
                     770                    775                    780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
                     785                    790                    795                    800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
                     805                    810                    815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
                     820                    825                    830  
 Ser Ala Lys Gly His His His His His His  
                     835                    840

<210> 260

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 260

atgaattccc tgcccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac 60





cagaccgcaa gctggatggt cggcggtcccc ccggaggccg tggacccctt gatgcgccgg 1980  
gcggccaaga cgggtgaactt cggcggtcctc tacggcatgt ccgcccatag gctctcccag 2040  
gagcttgcca tcccctacga ggaggcggtg gcctttatag agcgctactt ccaaagcttc 2100  
cccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg gggctacgtg 2160  
gaaacctctt tcggaagaag gcgctacgtg cccgacctca acgcccgggt gaagagcgtc 2220  
agggaggccg cggagcgcat ggccttcaac atgcccgtcc agggcaccgc cgcgcacctc 2280  
atgaagctcg ccatggtgaa gctcttcccc cgcctccggg agatgggggc ccgcatgctc 2340  
ctccaggtcg ccaacgagct cctcctggag gccccccaag cgcgggccga ggaggtggcg 2400  
gctttggcca aggaggccat ggagaaggcc tatcccctcg ccgtgcccct ggaggtggag 2460  
gtggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac 2514

<210> 261

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 261

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35				40					45				
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
		130				135					140				
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr
145					150					155					160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser
				165					170					175	

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
 180 185 190  
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg  
 195 200 205  
 Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys  
 210 215 220  
 Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys  
 225 230 235 240  
 Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val  
 245 250 255  
 Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala  
 325 330 335  
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu  
 405 410 415  
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala  
 450 455 460  
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg  
 500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr  
 530 535 540  
 Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg  
 725 730 735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala  
 770 775 780  
 Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala  
 785 790 795 800  
 Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro  
 805 810 815  
 Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly  
 820 825 830  
 His His His His His His  
 835

<210> 262  
 <211> 2526  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 262  
 atgaattcca ccccaactttt tgacctggag gaacccccca agcgggtgct tctggtggac 60  
 ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccggggggag 120  
 ccggtgcaga tgggtctacg cttcgcccgg agcctcctca aggccttgaa ggaggacgga 180  
 caggcggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag 240  
 gcctacaagg cgggcccggc cccacccccg gaggacttcc cccgccagct cgccttggtc 300  
 aagcggctgg tggaccttct gggcctggtc cgcctcgagg ccccggggta cgaggcggac 360  
 gacgtcctgg gcacctggc caagaaggcc gaaaggagg ggatggagg ggcgcatcctc 420  
 acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac 480  
 gggaccctgg tcaccccaaa ggacgtccag gagaagtacg ggtgcccc ggagcgctgg 540  
 gtggacttcc gcgccctcac gggggaccgc tcggacaaca tccccgggt ggcggggata 600  
 ggggagaaga ccgcccttcg actcctcgca gagtggggga gcgtggaaaa cctcctgaag 660  
 aacctggacc gggtaaagcc ggactcgctc cggcgcaaga tagaggcgca cctcgaggac 720  
 ctccacctct ccttagacct ggcccgcatc cgcaccgacc tccccctgga ggtggacttt 780  
 aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg 840  
 gagttcgga gcctcctcca cgagttcggc ctctctggag gggagaagcc ccgggaggag 900  
 gccccctggc ccccgccga aggggccttc gtgggcttcc tcctttccc caaggagccc 960  
 atgtggggcg agcttctggc cctggcgggc gcctcgggcg gccgcgtcca ccgggcccc 1020  
 gagccttata aagccctcag ggacctgaag gaggcgcggg ggcttctcgc caaagacctg 1080  
 agcgttctgg cctgagga aggccttggc ctcccgccc gcgacgacct catgctcctc 1140  
 gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcccgggc ctacggcggg 1200  
 gaggtagcgg aggaggcggg ggagcggg ccctttccg agaggctctt cgccaacctg 1260  
 cttaagaggc ttgaggggga ggagaggctc ctttggttt accgggaggt ggagaggccc 1320  
 ctttccgctg tcctggccca tatggaggcc acgggggtgc gcctggacgt ggcctatctc 1380  
 agggccttgt ccctggaggt ggccgaggag atcgcccgc tcgaggccga ggtcttccgc 1440  
 ctggccggcc accccttcaa cctcaactcc cgggaccagc tggaagggt cctctttgac 1500  
 gagctagggc ttcccgccat caagaagacg caaaagaccg gcaagcgctc caccagcgcc 1560





Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser  
 450 455 460  
 Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp  
 595 600 605  
 Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg  
 625 630 635 640  
 Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765









Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu  
 405 410 415  
 Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu  
 420 425 430  
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640  
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700



ggcagcctcc tccacgagtt cggcctcctg gaggcccccg cccccctgga ggaggcccc 900  
 tggccccgc cggaaggggc cttcgtgggc ttcgtcctct cccgccccga gcccatgtgg 960  
 gcggagctta aagccctggc cgcctgcagg gacggccggg tgcaccgggc agcagacccc 1020  
 ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc 1080  
 ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac 1140  
 ctcttgacc cctccaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtgg 1200  
 acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcgga cctccttaag 1260  
 cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gccctctcc 1320  
 cgggtcctgg ccacatgga ggccaccggg gtacggctgg acgtggccta ccttcaggcc 1380  
 ctttccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg 1440  
 ggccaccct tcaacctcaa ctcccgggac cagctggaaa ggggtgctctt tgacgagctt 1500  
 aggcttcccg ccttggggaa gacgaaaag acaggcaagc gctccaccag cgcgcgggtg 1560  
 ctggaggccc tacgggaggc ccacccatc gtggagaaga tcctccagca ccgggagctc 1620  
 accaagctca agaacaccta cgtggacccc ctccaagcc tcgtccaccg gaggacgggc 1680  
 cgcctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac 1740  
 cccaacctgc agaacatccc cgtccgcacc cccttggggc agaggatccg ccgggccttc 1800  
 gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc 1860  
 ctgccccacc tctccgggga cgaaaacctg atcagggtct tccaggaggg gaaggacatc 1920  
 cacaccaga ccgcaagctg gatgttcggc gtcccccccg aggccgtgga cccctgatg 1980  
 cgcggggcgg ccaagacggt gaacttcggc gtctctacg gcatgtccgc ccataggctc 2040  
 tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa 2100  
 agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc 2160  
 tacgtgaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag 2220  
 agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc 2280  
 gacctcatga agctcgccat ggtgaagctc ttccccgcc tccgggagat gggggcccg 2340  
 atgctcctcc aggtccacga cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400  
 gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gccctggag 2460  
 gtggaggtgg ggatggggga ggactggctt tccgccaagg gttag 2505

<210> 267  
 <211> 834  
 <212> PRT  
 <213> Thermus aquaticus

<400> 267

Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg  
130 135 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu  
145 150 155 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu  
195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp  
225 230 235 240

Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu  
245 250 255

Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg  
260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
275 280 285

Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro  
290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
305 310 315 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg

335

465

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780  
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800  
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
 805 810 815  
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
 820 825 830  
 Lys Gly

<210> 268  
 <211> 832  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 268  
 Met Glu Phe Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
 1 5 10 15  
 Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
 20 25 30  
 Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
 35 40 45  
 Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
 50 55 60  
 Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
 65 70 75 80  
 Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala





Leu Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu  
 450 455 460  
 Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg  
 725 730 735  
 Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
755 760 765

Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His  
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala  
785 790 795 800

Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro  
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala  
820 825 830

<210> 269  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 269  
gcgcggcggc ggggtgtggtg gttacgcgca gcgtgaccgc tacacttgcc agcgccctag 60  
cgc 63

<210> 270  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 270  
gcgctagggc gctggcaagt gtagcgggtca 30

<210> 271  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 271  
gatcgtgcg cgtaaccacc acaccgcgc cgcg 35

<210> 272  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 272  
ggactctgcc tcaagacggt agtcaacgtg 30

<210> 273  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 273  
cacgttgact accgtc 16

<210> 274  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 274  
catgtcaagc agtcctaact ttgaggcaga gtcc 34

<210> 275  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 275  
cagaccatga attccacccc acttttttgac ctggag 36

<210> 276  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 276  
gtggacgcgg ccgcccagg ccgcccagg ggccag 36

<210> 277  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 277  
cagaccatga tttccctgcc cctctttgag cccaag

36

<210> 278  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 278  
gtaaaccgcg ccgccacagg cggcggccaa ggcggtt

36

*Sub  
B  
Concluded*

004230 +0024550